


```

QY 411 KKLVTGKVLMAVSGSKRR-----KLRVYHCTNTDNPYEGDLTYAINTLHNV 461
D 337 KRLIGKVLAVNAGIQKRPGRVIRDLRLRYAACHNHNHNVYRGSITLFIINLHRSR 396
QY 462 KYLRLEPPSNQVQDQYKYLRLPLGPHGLSKSVQVNLGLTKMVDQDTLPPLMEKPLRGSS 521
D 397 KKLKAGTLRDLVLIQYLLQPYGGGLSKSVQVNLGLTKMVDQDTLPPLMEKPLRGRT 456
QY 522 LGLPAFSSFFVYIRNAKYAAC 542
D 457 LVIPVTMGFFVYKVNALAC 477

```

RESULT 2

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T45608
hypothetical protein F13G24.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear crease)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45608
R:Bayan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba
submitted to the Protein Sequence Database, December 1999
A:Reference number: 223009
A:Accession: T45608
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-521 <BBV>
A:Cross-references: UNIPROT:Q9SDA1; EMBL:AL133421
C:Experimental source: cultivar Columbia; BAC clone F13G24
C:Genetics:
A:Map position: 5
A:introns: 53/3; 66/1; 127/2; 177/1; 256/1; 319/2; 361/2; 394/3
A:Note: F13G24.30

```

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Query Match 14.6%; Score 416; DB 2; Length 521;
Best Local Similarity 29.2%; Pred. No. 5,8e-23;
Matches 154; Conservative 68; Mismatches 184; Indels 122; Gaps 24;

```

```

QY 75 LGSPLKRLIARGLSPAYLRFGGTKIDFLFPDKESTPEBSYMSQVNDICKYGSTPP 134
D 55 LTRPLTLTKAIKAKPKLRIRIGSLQDQVLYDVGNLKT-----PCR----- 94
QY 135 DVEBKRLKLEWYQEOQLREHYQKKPKNS--TYRSRSV-----DLYTFANCSGLDLIF 186
D 95 -----PFQKM-----NSGLFGFSKCLHMKRMDLNSFLTATGAVYTF 132
QY 187 GLNALRLRTADLQ-----MNSNSQAQLLDYCCKGNYI--SWELGNEPNSFLKKADIFIN 238
D 133 GLNALRGRHKLKRGKAMGAMDHINTQDPLNTYTSKGYTDSWEGNELSG--SGVGASVS 190
QY 239 GSQLQEDVITQLHKLIRKSTFPYNAKLYGPDVGP-----RRKTAFLKSLKAGGEVYDSV 293
D 191 AELYKDLIVLKDVINK--VYKNSWLHKRILVAFGFGFEQGYWTKLEI-----SGPSVADV 246
QY 294 TWHNYLYNGRT--ATREDFLNPVDLDFISSVQVVF-----QVVESTPGKVKVLTGTSBA 347
D 247 THNLYNIGSGNDPLLVKIKINDPS-----YLSQVSTFTFDVNOQTIOEHGPMASPVVGSBGA 302
QY 348 YGGGAPLILSTFPAAGFMWLDLGLSARMGILEVMRQVFGAGNYHVD--NRPDLPPYVL 406
D 303 YNSGGRHVSDTFLDSFYWYLDQLGMSARHNTKYVCRQIVG--GYGLLEKGTVPVNDYYS 361
QY 407 SLLEFKLVGTRVLMASVQSGKRRKRLRYLHCTNTDNPYEGDLTYAINTLHNV 464
D 362 ALIWHRLMGKGVLANVQIDGPP--QLRVYAHCSK-----GRAGVTLILLINISNQSDFTYS 413
QY 465 -----RLYPFS--NKQVDKYLRL--LGPBG--LLSKSVQL 495
D 414 VNSGINVVLNAESRKKKSLDLTKRPFWSIGKASGYANREHYHLPENGVYLSKSTIVL 473
QY 496 NGTLTKVNDQDTLPPLMEKPLRP--GSLGLPAFSSFFVYIRNAKYAAC 542
D 474 NGKSLKPLTATGDIPLS--EVLKSVNSPLNVLPLSMTSYLVLPNFDASAC 520

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RESULT 3

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T01953
hypothetical protein T2L5.6 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear crease)
C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01953
R:Geisel, C.; Smith, A.; Le, T.
submitted to the EMBL Data Library, October 1998
A:Description: The sequence of A. thaliana T2L5.
A:Reference number: Z14470
A:Accession: T01953
A:Status: translated from GB/EMBL/DDBT
A:Molecule type: DNA
A:Residues: 1-190 <GRT>
A:Cross-references: UNIPROT:O82604; EMBL:AF096371; NID:g3695386; PID:g3695392
C:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:introns: 36/2; 69/3
A:Note: T2L5.6
C:Superfamily: Arabidopsis thaliana hypothetical protein T2L5.6

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```

Query Match 6.0%; Score 169.5; DB 2; Length 190;
Best Local Similarity 27.8%; Pred. No. 2.5e-05;
Matches 54; Conservative 34; Mismatches 57; Indels 49; Gaps 9;

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QY 382 ROVFFGAGNYHVD--ENPDLPLDYWLSLFKLVGTGKVLMAVSGSKRRKRLRYLHCTNT 440
D 12 RSLTIG--GNVGLINTNTFPNPDYVSALIRQLMGRKALFTTFSGTK--KIRSYTHCA-- 66
QY 441 DNPYKSGDLTYAINTLHNV-----TKYLRLEPPSNQVQDQYKYLRL 483
D 67 ---RSQSG--ITVLNMLNNTTVAKVELNNSFSLRHKMK-----SYKASQLHG-- 115
QY 484 GPHGLL-----SKSVQNLGLTKMVDQDTLPPLMEKPLRGSSSLGPAFS 528
D 116 GPNVGIQREBHNLTKQGNLHLSQTMNLGNALQVNSMGDPLPEIPHINSTEPTIAPYS 175
QY 529 YSFFVYIRNAKYAAC 542
D 176 IVFVIMRNVVVPAC 189

```

RESULT 4

```

F64383
hypothetical protein M0670 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: F64383
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
reion, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; PMID:96337999; PMID:8688087
A:Accession: F64383
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-356 <BUL>
A:Cross-references: UNIPROT:Q58084; GB:U67514; GB:L77117; NID:g2826304; PID:AA89664.1;
A:Genetics:
A:Map position: REV596956-595886
A:Start codon: GTG

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Query Match 4.0%; Score 112.5; DB 2; Length 356;
Best Local Similarity 21.2%; Pred. No. 1.1;
Matches 85; Conservative 48; Mismatches 143; Indels 125; Gaps 18;
QY 126 ICKY-----GSIPDVEBKRLLEWYQEOQLLREHYQKKPKNSYRSVSD----- 171

```

Db 14 IRKMKIYNGKNEKDIKERLIKE-----LKEHVLEVETEDGTLYTLKADEEEMMSKV 66
QY 172 -----VLTPFANGSGLDLIFGLNALRTADLQNMSSNAQLLDYSSKGYNISWEIGNEP 226
Db 67 GALKKAIYFKAKPS-----KITDL-----SNPR-VLDLCSGKGYNAIALAHYMK 109
QY 227 NS-----FL-----KKADIFINGSQLEDYIQLHKLKSTF 258
Db 110 NAEIDMVEICEEVLFPLFLDIPYKEHEIHKQVKEFYLN-KIGREY-----KQDY 159
QY 259 KNAKLYGPDVGQPRKRTAKMLKSLKAGGEVIDSVTHHYLYNGRTAT-REDFLNPDLV 316
Db 160 DNINLY-----VGDAKRFIIKSDKKY-----NVFHDASFSPKPDPLYTYDFL----- 202
QY 317 DIFISVQKVPQVSTSTRGKVKWLGETSAYGGAPLISDFFPAGFMWLDLGLSARWG 376
Db 203 -----KEIYKQMEDN-GVLI-----SYSSAIPERSALVDCGFVISEKESVGRKKG 246
QY 377 IEVWRQVFFGAGNHLVDENFD-----PLPDYWLSLFFKKLVGTQVLMASVQSKXR 429
Db 247 ITLAKKNPKNFKNRINVEDERIALSVIALPYRDELISLTKKIIEDRERREKXKEKLI 306
QY 430 KLRVYLHCTNTDNPYKSGDLTLVA-INLHNVTKYLRIPY 468
Db 307 KIGKYLSTQIKKGNIPBEIILKIOKEDLNSSEIIKKMLKF 347
RESULT 5
T12094 beta-fructofuranosidase (EC 3.2.1.26) - fava bean
C/Species: Vicia faba (fava bean)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T12094
R/Weber, H.; Botisjuk, L.; Helm, U.; Buchner, P.; Mobus, U.
A/Title: Seed coat-associated invertases of Fava bean control both unloading and storage
A/Reference number: Z17416; MUID:96093423; PMID:8535137
A/Accession: T12094
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-575 <WEB>
A/Cross-references: UNIPROT:Q43855; EMBL:Z35162; NID:9861154; PIDN:CAA84526.1; PID:98611
A/Experimental source: cv. Fribo, seed coat
C/Genetics:
A/Gene: CMINV1
C/Superfamily: beta-fructofuranosidase
C/Keywords: cell wall; glycoprotein; glycosidase; hydrolase
Query Match 3.9%; Score 111.5; DB 2; Length 575;
Best Local Similarity 21.4%; Pred. No. 2.7; Indels 109; Gaps 19;
Matches 72; Conservative 48; Mismatches 107; Indels 109; Gaps 19;
QY 46 QEPHLVLS-----PSFLSVTIDANLATDPRFLILGSPKRLTLARGLS-----P 89
Db 228 KPIHSAKRTGMECEPDFFYPVSLGKNGLD--LSMMGNNVGHVKNLSIDITREYRYTIG 285
QY 90 AYLR-----FGTKTDF-----LIFDPKESTFEERSW---OSQVNG 124
Db 286 TYLQMDKXITPDKTSDEGGLRVDYGNFYAKSPFDDPK---NRIIIGWANSDDTKE 341
QY 125 DICKG-----SIPPDV-----EKKRLTEWPYQOQLLR-----EHYOKFKKSTYSRSRV 170
Db 342 DQVKGMAGIQAIPTVWLDSSRRQR-QMPVEELNRLRGQVEMKRLKXGGY----L 396
QY 171 DVLVTFPANGSGLDLIFGLNALRTADLQNMSSNAQLLDYSSKGYNISWEIGNEPNSFL 230
Db 397 EYKGITASQADVEVTFSSSLDKAEAFDPMENAE---DLCAQKSGSKVAGVG--PFGIL 451
QY 231 KKADIFINGSQLEDYIQL-----HKL-----RSTKNAKLYGP-----DV 268
Db 452 TLA-----SKLEETYSVFFRVFKANKGKILKMSDASSSILNRELKPSFAGFVNDL 505
QY 269 GQPRRTAKMLKSLKAGGEVIDSVTHHYLYNGRT 304

Db 506 GNNKLSIRSL-----IDHSVSESFFVGGRKT 531
RESULT 6
T10666 hypothetical protein F6E21.40 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T10666
R/Beyan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro
submitted to the Protein Sequence Database, June 1999
A/Reference number: Z16533
A/Accession: T10666
A/Molecule type: DNA
A/Residues: 1-670 <BY>
A/Cross-references: UNIPROT:Q9M090; EMBL:AL049914; GSPDB:GN00062; ATSP:F6E21.40
A/Experimental source: cultivar Columbia; BAC clone F6E21
C/Genetics:
A/Map position: 4
A/Intons: 47/3; 87/1; 123/3; 203/3; 230/2; 255/3; 284/3; 305/1; 335/3; 347/3; 370/3; 39
C/Superfamily: Schizosaccharomyces pombe negative regulator of mitosis bkl1
Query Match 3.9%; Score 111; DB 2; Length 670;
Best Local Similarity 22.4%; Pred. No. 3.7; Indels 156; Gaps 33;
Matches 123; Conservative 77; Mismatches 194; Indels 156; Gaps 33;
QY 51 LVSPSFLSVTIDANLATDPRFLILGSPKRLTLARGLSPAY-LRFGTKTDFLIIPDK- 107
Db 47 LVDPSPRLSVEGN-GVDTQVLPVCGSDLV-----LSPSQMSSHVGVKISSWIDLDSBD 99
QY 108 -----KESTFEERSWYQSONNODICKXGSI-PPDVEKRLRLEVPYQEQQLLREHYQKKFK 161
Db 100 EYLRMDSTTLKQELAMATHLSLQMC-----PD-----LRPHLAGL 139
QY 162 NSTYSSRSV---DVLX-----TFANCS---GLDLIFGLNALRTADLQNMSSNAQL 207
Db 140 RVSCCRSSFIDETFLVITFNQALTFCGSSILFCNLVIALKMLRVPLV---SEGDSM 196
QY 208 LDYSSKGYNISWEIGN-----EPNSFLKKA-DIFIN-----GSQLEDYIQLHKL 253
Db 197 DD--TSBGLNDSWEIWMNSFRLLCEHDSYLSVALDVLSTLPSETSLGRWVGES-VRAATLS 253
QY 254 RSTFKNAKLYGPDVGQPR-RRTAKMLKSL-KAGGEVIDSVTHHYLYNGRTATREDF 310
Db 254 TDAFLTNAR-----GYCLSKRHQKLAGFPDHAQVVICGPVHNLQKPLDSSSEGT 307
QY 311 LNPDLIDFISVQKVPQVSTSTRGKVKWLGETSAYGGAPLISDFFPAGFMWLDKLG 370
Db 308 KNP--LRITYLVVATLPQKMSLSQERIEIGYRFLQAPLDPLMDNLEAQYETFE--- 362
QY 371 LSARNGIEVWRQVFFGAGNHLVDENFDPLPDYWLSLFFKKLVGTXYLM----- 420
Db 363 ---RDSVXIYQ---RAVERKALVDR---VPDEKASEL-----TYLMMVVGAGRGPLY 406
QY 421 -ASVQSGSR--RKLRYVLHCTNTDNPYKSGDLTLIYALNINLVTK-----YLRLPY 468
Db 407 RASLQAAETDRKLVY---AVEKNPN-----AVVTLNHLVMEGMEDEVYTIISCDM 455
QY 469 PFSN--KQVDKYLRLPLPHGLSKSVQNLGTLTMVDDQTLPLM---EKLPRGSSSIG 523
Db 466 RFWMNPRQADILVSLGSGF-----DNEISPECLDGAQRRLK--DGIS 498
QY 524 LPAPSYSPFV 533
Db 499 IPS-SYTSFI 507
RESULT 7
S32961 hypothetical protein YBR259w - yeast (Saccharomyces cerevisiae)
N/Alternate names: hypothetical protein YBR127

[illegible]

```

Qy      369 IGLSNR-MQIEVVMRQVFGAGNYHL--VDENEDPLPDYLSL-LFKKLVG--TKVL--- 419
Db      1756 IIKPKRFLEIETVYLAIVLQQRGLPFLAEADVSAKMTPEYDNIHLDFSRALHYMKRLRG 1815
Qy      420 -----MASVQSK-----RRKILRVYLHCNTNTDNPRTYKKEGDLTLVYAINLHNVTYKL 464
Db      1816 ATTPAAGVTSASSTAGSSSAQIRKQREEPSH----- 1847
Qy      465 RLPYPPSKQVDKYLLRPLG-----PHGLLSKSYQLAGLTITKMD-- 504
Db      1848 TLQLAMTNINKQLFLRLSLALADPTASSTEHRDYNAFTTGLIS-LIKSGVGIVVDSF 1906
Qy      505 -----DQTLPLIMEKPLRPG-----SSLGAPAFSYSF-FVIRNAKYA 540
Db      1907 FLTPDSYSPLQDPQLHTAGIMAYGVRLSEKQVPAASQLFWLFFNNFKYA 1957

RESULT 9
E91031
probable outer membrane protein Ecs3221 [imported] - Escherichia coli (strain O157:H7, su
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: E91031
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gsawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genor
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: E91031
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-879 <HAY>
A:Cross-references: UNIPROT:G8XCP4, GB:BA000007, PID:BA93664.1, PID:91362691, GSPDB:GI
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: Ecs3221

Query Match      3.9%; Score 109.5; DB 2; Length 879;
Beef Local Similarity 20.1%; Pred. No. 7.3; 208; Indels 241; Gaps 33;
Matches 130; Conservative 68; Mismatches 241; Gaps 33;

Qy      52 VSPFLSVITDNLITDPRFLITLGSFKLRTIARGLSPAYLRFGGTITDPLIPDKKEST 111
Db      20 MSGSYVNAIAEKRIQDFSRFLTKGDPDKI-DLKRFSQGVBERG--KYNLOVOVKRQPLT 76


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QY	112	FEERSYMSQVONADICTGSIIPDPVEEKL-----RLPMYQOBQLLREHYOKKFRNS	163
Db	77	BEYDIYMWASENDASKTYACTLPPELVAOCGLKEDYAKNIQWIDHGCLTKRGQLE-----	130

Oy	164	YRSMSSVUVLYTFPANCSEGLDIFGI-NALLTATLQNMSSN-----	AQLLDVC-----	211		
Db	131	-----GIDIK---ADLSQSALVVISLPQAYVLETTIDNMPPSRMDGISGLTADYSTAQT		182		
Oy	212	-----SSKGYNI-SWEI-GNEPNSFL---KKADIFINGSQ-----		241		
Db	183	RHEENGDDSDSNEISGNGVGNLGAHKLRLAMQOTDIYHKSNDVVDVINGDDTQKNMEWR		242		
Oy	242	-----LGEDYIQLHKLRLKSTF-----	XNAKLYGBDV	268		
Db	243	YYAWRALPSLKAUKLGLGEDY-----LNSDIFDGNVYGSISTDDQWLPEHLGVAADI		296		
Oy	269	GQPRKTKAKMLKSLFKACGEVI-----	DSYTHHHYLANGRTATREDPLN	312		
Db	297	SGVAHTTKAVVSQL---GRAVITYETQVAPGPFRIODLDSV-----	SGTLHTRIEON	346		
Oy	313	PDVLDIFASSQVKVQVVESTRPGK---KMWL-----	GETS-----	345		
Db	347	GOVDEYDINTLSMPF---LTPRGQVRXYKLMMGRPEQKGGHHVEGGFBSGGSAWSGIANGW		402		
Oy	346	SAYGSGAPLLSD-----	TFEA-----	GFWMLDKL-----	GLSAR	374
Db	403	SLYXGA---LADENHYGSAALGVGRDLSVFGAVADPITHSHTRLDKETAHYGKSLDGNMFR		459		
Oy	375	MGI-----EVMVROVFFGAGNYHLVDENEDPLPDYWLISLFLKLVGT---	YVLMAVQGS	426		
Db	460	LSYSKDPFELMSRVTJFAG---YRFSEENFMTMSEX-LDASDEMYRGTGNDKEMYTATVQN		515		
Oy	427	KRRKLRYVLIHCTNDNPRYKEGDLTLVAI-----	NLHNVTK-----	462		
Db	516	NFRDAGSVVLYNTRHTYWRDREQTNVVMVLSHYFNLSISIRNMSISMTGYREYEDNOADK		575		
Oy	463	--YLRLPYPSFNKQVDKYLLRLPLGPHGLSKSVOLNGTLKMGVDDQT		507		
Db	576	GVIYISLSMPGSDSSTISY---NGNYGSGSDSQVG---YFSRRVDAT		616		

RESULT 10
574760
hypothetical protein slr1617 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: 574760
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
S. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-116, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
5.
A:Reference number: 574332; PMID:97061201; PMID:8905231
A:Accession: 574760
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1411 <KAN>
A:Cross-references: UNIPROT:P72895; EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BA1691;
/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

```

Query March 3.8%; Score 108.5; DB 2; Length 411;
Beet Local Similarity 21.4%; Pred. No.2.7;
Matches 66; Conservative 55; Mismatches 94; Indels 93; Gaps 17;

QY KFNSTYRSRSDVLTVPANCSGDLTF--GLNALLRTADLQWNSNAOL-----206
Db EFRLLISPPREQIDI---FAGSTKDDLASEENIDICIVHLANPRVYTSVVMAGGUTLIMRN 207

QY LLDYCSGSG---YNISWEL-----GNEPNSFLKK-----ADIFINGSQDGE 244
Db VIDVCLADIDILYPPSSWEIYSYGAGTIHADSEFTALRCPGYGKTYLAETLI-----260

QY DYIGLHLKRTSTFNKATLYGPDVCGQPRKRTAKMLKSLKLGAGEVIDSVTMHHVYILNRT 304
Db DHCRTRKRLCAIILKSSPVYGSMSDKP---KLFNFKPKASGGQKIVT--HHYING-- 311

```

```

QY 305 ATREDFNPEDV-----LDIFISSVQKVPQWESTRGKKVMIGETSATSAVGGAPLSDTFA 360
Db 312 -----NPKDLHLHIDPLISSIVATL-----KSRFNLNLT-----GGQQLSTLK 351
QY 361 AGFMWLDLGLSA-----RMGIEVVMROVFPFGAGNYHLVDENFDPLDYWLISLLFKKLVG 415
Db 352 IAEMLRDELSSSMIQOLEVNTVEVASIANYGRAN-HVLD-----WEVYIFEE-QG 400
QY 416 TKVLASV 423
Db 401 LKSLIHQI 408

```

RESULT 11
D87541
beta-xyloridase [imported] - Caulobacter crescentus
C|Species: Caulobacter crescentus
C|Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C|Accession: D87541
R|Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Ijau, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Esmola, M.T.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A|Title: Complete Genome Sequence of Caulobacter crescentus.
A|Reference number: A87249; MUID:21173698; PMID:11259647
A|Accession: D87541
A|Status: preliminary
A|Molecule type: DNA
A|Residues: 1-500 <STO>
A|Cross-references: UNIPROT:Q9A5U0; GB:AE005673; NID:g13423886; PIDN:AK24328.1; GSPDB:G
C|Gene: CC2357

	Query Match	Similarity	Score	DB 2	Length	500;
Best	Local	Similarity	25.7%	Pred. No.	4.4;	
Matches	56;	Conservative	35;	Mismatches	80;	Indels 47; Gaps 15;
Qy	165	YSRSSVDVLYTEANCSEGLDILFGLN--ALLRTAD--LOW--NSSNAQL-----LLD--	209			
Db	81	YDWTIKIDQLDYDALLAKGIRPFIELGFTPEAMKTSDDTI FFWKGTSTSHPKLGPMWRDLIDAF	140			
Qy	210	-YCSEKGVNI-----SW--ELGNEPN--SPLKKKDIFINGSQLGSDYIOLHTLKRSTFKN	260			
Db	141	VHHLFARYGVEEVRTTFEEVWNEPNLDGFWEKAD-----QAAYPEFLYDV---TARA	188			
Qy	261	AKLYGPD--VGQPRRTAKLXSLF--KAGEVIDSVTMHHYLYNG--RTATREDFL	311			
Db	189	IKAIIDPSLRTVGCPATAGAAVPEFLAHVKKSGSAVDVTTHTTYGVDCGFLDEKGVQDTKL	248			
Qy	312	NPDVLDIFISSVQKVFQVVE--STRPKKWLIGSTSSAY	348			
Db	249	SPSP--DAVGVDRVRKEQLEASAFPGGLPLFTFESTSY	285			

RESULT 12
P85875
probable fimbrial usher Z3600 [imported] - Escherichia coli (strain O157:H7, substrain E
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: F85875
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.U.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouzis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; M0ID:21074935; PMID:11206551
A:Accession: F85875
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-879 <STO-
A:Cross-references: UNIPROT:O8XCP4; GB:AE005174; NID:G12516702; PIDN:AGS7466.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Gene: Z3600

A:Gene: ADE1; SPDB:SPBC405.01

A:Map position: 2

C:Superfamily: Saccharomycetes cerevisiae ADE5 multifunctional protein, phosphoribosylamin

C:Keywords: cyclo-ligase; purine nucleotide biosynthesis
F/5-425/Domain: phosphoribosylamine-glycine ligase homology <PGL>
F/439-767/Domain: phosphoribosylformylglycinamide cyclo-ligase homology <PFCU>

Query Match 3.7% Score 104.5; DB 1; Length 788;

Best local similarity 27.7%; Pred. No. 15; Mismatches 114; Indels 33; Gaps 11;

Matches 70; Conservative 36; Mismatches 114; Indels 33; Gaps 11;

Qy 297 HYLNGRTATRE--DFLNPDV-LDIFISSVQKVFQVEST--RPGKKWLGSTSSAY----- 348

Db 424 HVALNPKKTRRELIVENSGVVDNGNEFQRIKDLVSTRPADADIGCGGIFDLKQ 483

Qy 349 -GGAPLL-SDTFPAAGFMWLDKLGSLAR--NGIEVVMQVFFGAGNYHLVDENPDL--P 402

Db 484 AGMNDPLVVSATDVGSKLLIALSLNKHDTVGIDLVAMNV-----NDLVVQGAEPILFL 537

Qy 403 DYWLSLFRKLVGTQVLMASVQSGSRKRLRVYHCTNTDNPYKXEGDLTLVAINLHNTX 462

Db 538 DVFATGSLDKVSTSFVEGVNKGCKQAGCALVGSTSEMPGLYHDGHYDANGTSVGAISR 597

Qy 463 YLRLPYPSNKQVDKYLRLRPLGPHGLSKSVQNLGLTL--KMVD-----DQTLPLMERPL 516

Db 598 DDILPKPESFSGKDLIL-----GLASDGVHNSNGSLVRKIVEYSDLEYTSVCPMDKNV 650

Qy 517 RFGSSLGLPAPSY 529

Db 651 RLGDSLILPTRY 663

RESULT 15

F70411

adenylosuccinate synthetase - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C:Accession: F70411

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O

V.

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: F70411

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-432 <AQP>

A:Cross-references: UNIPROT:067321; GB:AE000733; NID:g2983720; PIDN:AA07286.1; PID:g298

A:Experimental source: strain VPS

C:Genetics:

A:Gene: purA

C:Superfamily: adenylosuccinate synthase

Query Match 3.7% Score 104; DB 2; Length 432;

Best local similarity 23.9%; Pred. No. 6.4; Mismatches 128; Indels 138; Gaps 22;

Matches 96; Conservative 39; Mismatches 128; Indels 138; Gaps 22;

Qy 15 LLLGLPLGLSPGALPRPAQADVVDL-----PFTQEPHLVSPS 55

Db 51 ILHLPTGILHSHVGVIAQGM-VVDLEVLHKEVNLEKGIYKERLFISDRALHVPY 109

Qy 56 FLSTVITDNLATDPRFLILGSPK--LRTLAGLSPAYL-RFGCTKTDFLIPDPKKESTF 112

Db 110 H-----KLLDLSLFEKKKGIGITTLRGIGAPVAFKY--RKGIKISDLKDEKRF 154

Qy 113 EERSYQSOVNODICKYGSIPDVEEK-----LRLWPYQEQLLREHYQKFKNSTY 165

Db 155 -----YTLLEDNDLPK-----NICEKVCCEKFDLDINOIYEQI-----RYFEKENV- 199

Qy 166 SRSSVDVLYTFANCSGLDILFGLNALRTADI-----QNNSSNAQLLDYCSSKGYNISWE 221

Db 200 ---VDLLRFNTQKGSVLFEGAGQTLIDVDWGTVPYVTSSNASAL-----GLSNG 246

Qy 222 LGNEPNSFLKKADIFING-----SQL-GE DYIOLHKLRLKSTFNQAKLYG 265

Db 247 TGMPPKYF---SDAFILGVAKAYTTRVGEFPFTELKGBEGBKRLREL-----GGEYG 295

Qy 266 PDVQPRR--KTAKMLKSLKAGGEVIDSVTHHYLYNGRTATREDPLN----- 313

Db 296 STTGRPRRCGWLIDVALKXAVQVNG-----LDGFVITKLDVLDTFDEVKVCVA 343

Qy 314 -----DYLDIFISSVQKVFQV--VSTRPGKKWLGSTSSA 347

Db 344 YELDEVIDYFPASYSBLIRKVPYKTLKG--WKGSTKGA 381

Search completed: February 28, 2005, 05:53:41
Job time : 48 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 28, 2005, 05:52:46 ; Search time 180 Seconds
(without alignments)
1544.772 Million cell updates/sec

Title: US-10-786-149-2

Perfect score: 2842

Sequence: 1 MLRSKALPPLMLLLGP.....LPAPSPFVIRNKAACI 543

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2838	99.9	543	2	Q9Y251
2	2817	99.1	545	2	Q9UL39
3	2282	80.3	545	2	Q9MYT0
4	2150	75.7	535	2	Q8K3K3
5	2140	75.3	535	2	Q6Y3Z1
6	2135	75.1	536	2	Q7LRP1
7	2123	74.7	523	2	Q9QZP8
8	1645.5	57.9	523	2	Q9QYK5
9	1154.5	40.6	592	2	Q9HB37
10	1146.5	40.3	592	2	Q8WQ02
11	1015.5	35.7	548	2	Q8WQ01
12	936.5	33.0	534	2	Q9HB38
13	897.5	31.6	480	2	Q9HB39
14	696	24.5	515	2	Q8T108
15	416	14.6	521	2	Q8SDA1
16	416	14.6	543	2	Q9FF10
17	404	14.2	559	2	Q89FP9
18	392.5	13.8	544	2	Q8H615
19	381	13.4	527	2	Q9LR08
20	379	13.3	541	2	Q691T5
21	364	12.8	537	2	Q70YU3
22	363	12.8	536	2	Q9FZP1
23	352.5	12.4	516	2	Q9FLK8
24	352.5	12.4	539	2	Q8L608
25	350.5	12.3	529	2	Q6ZJ02
26	169.5	6.0	190	2	Q8Z604
27	160	5.6	935	2	Q9YE79
28	141	5.0	559	2	Q7SFB0
29	136.5	4.8	463	2	Q63T97
30	130.5	4.6	493	2	Q9HK01
31	122.5	4.3	408	2	Q9HE21

32	122.5	4.3	408	2	Q9HE22	Q9he22 phanerochaete
33	116.5	4.1	169	2	Q40996	Q40996 measles vlr
34	114.5	4.0	1167	2	Q869K5	Q869K5 dictyostell
35	114	4.0	398	2	Q72RP7	Q72rp7 leptospira
36	114	4.0	398	2	Q8F410	Q8f410 leptospira
37	113.5	4.0	617	2	Q83295	Q83295 measles vlr
38	113.5	4.0	1829	2	Q9KH44	Q9kh44 pantoea agg
39	113	4.0	390	2	Q8TPH7	Q8tph7 methanocarc
40	112.5	4.0	356	1	Q570.METUA	Q56084 methanococc
41	112.5	4.0	617	2	Q83647	Q83647 measles vlr
42	112	3.9	732	2	Q7MSD4	Q7msd4 wolinnella b
43	111.5	3.9	493	2	Q979W0	Q979w0 thermoplasm
44	111.5	3.9	575	2	Q43855	Q43855 vicia faba
45	111.5	3.9	617	2	Q40991	Q40991 measles vlr

ALIGNMENTS

RESULT 1

ID	Q9Y251	PRELIMINARY;	PRT;	543 AA.
AC	Q9Y251			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)		
DT	25-OCT-2004	(TREMBLrel. 28, Last annotation update)		
DE	Heparanase.			
GN	Name=HPA; Synonyms=HPSE;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=99332149; PubMed=10395326;			
RA	Hulett M.D., Freeman C., Hamdorf B.J., Baker R.T., Harris M.J.,			
RA	Parish C.R.;			
RT	"Cloning of mammalian heparanase, an important enzyme in tumor			
RT	invasion and metastasis."			
RL	Nat. Med. 5:803-809(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=99335379; PubMed=10405343; DOI=10.1006/bbrc.1999.0962;			
RA	Kuesie P.H., Holmes J.D., Ludwig D.L., Patel S., Navarro E.C.,			
RA	Seddon A.P., Giorgio N.A., Bohlen P.;			
RT	"Cloning and functional expression of a human heparanase gene."			
RL	Biochem. Biophys. Res. Commun. 261:183-187(1999).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99377052; PubMed=10446189; DOI=10.1074/jbc.274.34.24153;			
RA	Toyoshima M., Nakajima M.;			
RT	"Human heparanase. Purification, characterization, cloning, and			
RT	expression."			
RL	J. Biol. Chem. 274:24153-24160(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Pancreas;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,			
RA	Altech S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh P.,			
RA	Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ueda T.B., Toshiyuki S., Carinci P., Prange C.,			
RA	Baba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,			
RA	Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,
RT Jones S.J., Maitra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.,
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Vlodavsky I., Friedman Y., Elkin M., Aingorn H., Arzamon R.,
RA Ishaï-Michaeli R., Bitan M., Pappo O., Peretz T., Michael I.,
RA Spector L., Becker I.,
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF165154; AAD45379.1; -
DR EMBL; AF152376; AAD45669.1; -
DR EMBL; AF155510; AAD54941.1; -
DR EMBL; BC051321; AAH51321.1; -
DR EMBL; AF144325; AAD41342.1; -
DR GO; GO:0004566; Fibroblast growth factor activity; TAS.
DR GO; GO:0006023; Fibroblast growth factor receptor activity; TAS.
DR InterPro; IPR005199; Glyco_hydro_79n; 1.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
FT CHAIN 158 543 heparanase.
SQ SEQUENCE 543 AA; 61176 MW; AD262EC267334AB2 CRC64;
Query Match 99.9%; Score 2838; DB 2; Length 543;
Best Local Similarity 99.8%; Pred. No. 1.9e-204;
Matches 542; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDLDFPTQEPHLVSPSFLSVT 60
DB 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDLDFPTQEPHLVSPSFLSVT 60
QY 61 IDANLATDPRLILGLSPKRLTLARGLSPAYLRFGTKTDFLLPDKKESTFEERSYQS 120
DB 61 IDANLATDPRLILGLSPKRLTLARGLSPAYLRFGTKTDFLLPDKKESTFEERSYQS 120
QY 121 QVNODICKYGSIPDVEEKLRLMPYQEQLLREHYQKKFKNSYSSVDVLYTFANCS 180
DB 121 QVNODICKYGSIPDVEEKLRLMPYQEQLLREHYQKKFKNSYSSVDVLYTFANCS 180
QY 181 GIDLIFFGLNALIRFADLQWSSNAQLLDYCSSKGYNISWELGNBPNSFLKKADIFINS 240
DB 181 GIDLIFFGLNALIRFADLQWSSNAQLLDYCSSKGYNISWELGNBPNSFLKKADIFINS 240
QY 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRKRTAKMLKSLKAGGEVIDSVTMHHY 300
DB 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRKRTAKMLKSLKAGGEVIDSVTMHHY 300
QY 301 NGRTATREDPLNDVDLFISSVQKYPQVVESTTRPGKRWLGETSSAYGGAPLSDT 360
DB 301 NGRTATREDPLNDVDLFISSVQKYPQVVESTTRPGKRWLGETSSAYGGAPLSDT 360
QY 361 AGFWMLDKLGLSARMGIEVVMROVFGAGNYHVDENFPLDPYMLSLFKKLVGTRKV 420
DB 361 AGFWMLDKLGLSARMGIEVVMROVFGAGNYHVDENFPLDPYMLSLFKKLVGTRKV 420
QY 421 ASVQSGRRKRLRYVLIHCTNTDNPYKEGDLTYAINHNTYKRLRPYPSNQVDKYL 480
DB 421 ASVQSGRRKRLRYVLIHCTNTDNPYKEGDLTYAINHNTYKRLRPYPSNQVDKYL 480
QY 481 RPLGPHGLLSKSVQNLGLTKMVDQTLPLMEKPLRPSSGLPAFYSFFVIRNAKYA 540
DB 481 RPLGPHGLLSKSVQNLGLTKMVDQTLPLMEKPLRPSSGLPAFYSFFVIRNAKYA 540
QY 541 ACI 543
DB 541 ACI 543

RESULT 2
Q9UL39
ID Q9UL39 PRELIMINARY; PRT; 545 AA.
AC Q9UL39;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Heparanase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20229546; PubMed=10764835; DOI=10.1093/glycob/10.5.467;
RA Dempsey L.A., Plummer T.B., Coombes S.L., Platt J.L.,
RT "Heparanase expression in invasive trophoblasts and acute vascular
RT damage.",
RL Glycobiology 10:467-475 (2000).
DR EMBL; AF084467; AAD54516.1; -
DR Genew; HGNC:5164; HPSE.
DR InterPro; IPR005199; Glyco_hydro_79n; 1.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 545 AA; 61417 MW; 67B80ACD73C5A9A1 CRC64;
Query Match 99.4%; Score 2817; DB 2; Length 545;
Best Local Similarity 99.4%; Pred. No. 7.1e-203;
Matches 542; Conservative 1; Mismatches 0; Indels 2; Gaps 2;
QY 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDLDFPTQEPHLVSPSFLSVT 58
DB 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDLDFPTQEPHLVSPSFLSVT 58
QY 59 VTIDANLATDPRLILGLSPKRLTLARGLSPAYLRFGTKTDFLLPDKKESTFEERSY 118
DB 61 VTIDANLATDPRLILGLSPKRLTLARGLSPAYLRFGTKTDFLLPDKKESTFEERSY 120
QY 119 QSVNODICKYGSIPDVEEKLRLMPYQEQLLREHYQKKFKNSYSSVDVLYTFAN 178
DB 121 QSVNODICKYGSIPDVEEKLRLMPYQEQLLREHYQKKFKNSYSSVDVLYTFAN 180
QY 179 CSGDLIFGLNALIRFADLQWSSNAQLLDYCSSKGYNISWELGNBPNSFLKKADIFIN 238
DB 181 CSGDLIFGLNALIRFADLQWSSNAQLLDYCSSKGYNISWELGNBPNSFLKKADIFIN 240
QY 239 GSGLEDYIQLHKLRLKSTFKNAKLYGPDVGQPRKRTAKMLKSLKAGGEVIDSVTM 298
DB 241 GSGLEDYIQLHKLRLKSTFKNAKLYGPDVGQPRKRTAKMLKSLKAGGEVIDSVTM 300
QY 299 YNGRTATREDPLNDVDLFISSVQKYPQVVESTTRPGKRWLGETSSAYGGAPLSDT 358
DB 301 YNGRTATREDPLNDVDLFISSVQKYPQVVESTTRPGKRWLGETSSAYGGAPLSDT 360
QY 359 FAAGFWMLDKLGLSARMGIEVVMROVFGAGNYHVDENFPLDPYMLSLFKKLVGTRKV 418
DB 361 FAAGFWMLDKLGLSARMGIEVVMROVFGAGNYHVDENFPLDPYMLSLFKKLVGTRKV 420
QY 419 LMASVQSGRRKRLRYVLIHCTNTDNPYKEGDLTYAINHNTYKRLRPYPSNQVDKYL 478
DB 421 LMASVQSGRRKRLRYVLIHCTNTDNPYKEGDLTYAINHNTYKRLRPYPSNQVDKYL 480
QY 479 LRLPGLPHGLLSKSVQNLGLTKMVDQTLPLMEKPLRPSSGLPAFYSFFVIRNAKYA 538
DB 481 LRLPGLPHGLLSKSVQNLGLTKMVDQTLPLMEKPLRPSSGLPAFYSFFVIRNAKYA 540
QY 539 VAACT 543
DB 541 VAACT 543

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RESULT 3
Q9MYX0 PRELIMINARY; PRT; 545 AA.
ID Q9MYX0
AC Q9MYX0
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Heparanase.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Kumlantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=21176669; PubMed=11277877;
RA Kizaki K., Nakano H., Nakano H., Takahashi T., Imai K., Hashizume K.;
RT "Expression of heparanase mRNA in bovine placenta during gestation.";
RL Reproduction 121:573-580(2001).
DR EMBL; AF281160; AAF87301.2; -
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; I.
SQ SEQUENCE 545 AA; 61076 MW; FAF4BDPFD855B933 CRC64;

Query Match 80.3%; Score 2282; DB 2; Length 545;
Best local similarity 79.8%; Pred. No. 1,1e-162;
Matches 435; Conservative 35; Mismatches 73; Indels 2; Gaps 1;

QY 1 MLRSKPALPPPLML--LIGPLGSLPGALPRPAQADVLDPTFQEPHLVSPFLS 58
DB 1 MLACRKPELRPPLLLPLGLGPGCSPTAAAAADDAALDEFERPHLVSPFLS 60
QY 59 VTIDANLATDRPRLILGSPKLTARGLSPAYLRFGGTCTDFLIFDKKSTPERKSYW 118
DB 61 FTIDANLATDRPRLILGSPKLTARGLSPAYLRFGGTCTDFLIFDKKSTPERKSYW 120
QY 119 OSQVNDICCKYGSIPDVVEEKLRLMPYQEOILLREHYQCKKSTYSSVADVLYTPAN 178
DB 121 LSGNSODICCKSGSLPSDVEEKLRLMPYQEOILLREHYQCKKSTYSSVADVLYTPAN 180
QY 179 CSGDLIFGLNALRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 238
DB 181 CSGDLIFGLNALRTADLQWNSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFIN 240
QY 239 GSQIGEDYIQHLKLRKSTFKNAKLYGPDVQPRPKTKAMLKSPFKAGGEYIDSTWIMHY 298
DB 241 GROLGEDEIFERRKLLGKSAFKNAKLYGPDVQPRPKTKAMLKSPFKAGGEYIDSTWIMHY 300
QY 299 YLNRRTAREDFLNPDDVDIFISSVQKYFOVVESTRPKKXWLGFTSAGGAPLISDT 358
DB 301 YLNRRTAREDFLNPDDVDIFISSVQKYFOVVESTRPKKXWLGFTSAGGAPLISDT 360
QY 359 FAAGFMWLDKLGSARMGIEVVMRQVFGAGNYHLVDENFPLPDYWLSTLFFKLVGTGV 418
DB 361 FAAGFMWLDKLGSARMGIEVVMRQVFGAGNYHLVDENFPLPDYWLSTLFFKLVGTGV 420
QY 419 LMASVQSKRRRLRYLHCTNTDNPRYKGGDTLYAIVLHNVTKYLRPYPSNKQVDYK 478
DB 421 LMASVQSKRRRLRYLHCTNTDNPRYKGGDTLYAIVLHNVTKYLRPYPSNKQVDYK 480
QY 479 LLRLPGHPGLSKSVQNLGLTKWDDOTLPLMKKPLRPSSSGLPAPFSYSPFIRNAK 538
DB 481 LLRLPGHPGLSKSVQNLGLTKWDDOTLPLMKKPLRPSSSGLPAPFSYSPFIRNAK 540
QY 539 VAACI 543
DB 541 VAACI 545

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Q8K3K3;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Heparanase (Mus musculus 0 day neonate thymus cDNA, RIKEN full-length
DE enriched library, clone:A430101M04 product:heparanase, full insert
DE sequence).
CN Name=Hpsae; Synonyms=Hpa, Hape;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB;
RA Miao H.-Q., Navarro E., Patel S., Sargent D., Koo H., Wan H.,
RA Plata A., Zhou Q., Ludwig D., Bohnen P., Kissele P.;
RT "Cloning, expression, and purification of mouse heparanase.";
RL Protein Expr. Purif. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=20349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata K., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Azawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitahara T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto K., Matsuno H., Sakaguchi S., Ikegami T., Kaishogi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Azawa K., Akiyama T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Koda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

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RA Nishi K., Nomura K., Numazaki R., Ohno M., Ono N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
 RU Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUJ/J; TISSUE=Spleen;
 RA Hallet M.D., Wang J., Hornby J.R., Freeman C., Pagler E., McHenry J.,
 RA Parish C.R.,
 RU Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY077467; AAL76083.1; -
 DR EMBL; AF040471; BAC30600.1; -
 DR EMBL; AF359507; AA015188.1; -
 DR MGD; MGI:1343124; HpaII.
 DR GO; GO:0005788; C:extracellular matrix (sensu Metazoa); TAS.
 DR InterPro; IPR005199; Glyco_hydro_79N.
 DR Pfam; PF03662; Glyco_hydro_79n; 1.
 DR SEQUENCE 535 AA; 60065 MW; 6E73A8302FB8A0DF CRC64;
 SQ
 Query Match 75.7%; Score 2150; DB 2; Length 535;
 Best local Similarity 76.6%; Pred. No. 8.9e-153;
 Matches 407; Conservative 51; Mismatches 73; Indels 0; Gaps 0;
 QY 13 LMLLLGPIGLSPGALPRPAQADVDVDFDFTQEPHLIVSPFSLVTIDANLATDPRFL 72
 DB 5 LILMLMGPIGLALAGAPAGTAPTDVDFEFTYKRLRSVSPFSLITIDASTADPRFL 64
 QY 73 ILLGPKRLTARGLSPAYIRFGTKTDFLIPDKKESTFEERSYVQSQVNOIDCKYGS1 132
 DB 65 TFLGSPRLALARGSPAYIRFGTKTDFLIPDKKESTFEERSYVQSQVNOIDCKRBPV 124
 QY 133 PPVBEKRLRLEWVYQEOILLREHYOKFKFNSTYSRSVDVLYTFANCGSLDIFGINALL 192
 DB 125 SAAVLRKLVQWEPFQELLRLREYQKFKFNSTYSRSVDVLYTFANCGSLDIFGINALL 184
 QY 193 RTADLQNNSSNAQLLDYCSSKGNISWELGNEPNSFLKKAIDIFINGSQIGEDYIOLHKL 252
 DB 185 RTPDLRNNSSNAQLLDYCSSKGNISWELGNEPNSFWKKAHLLIDGLQIGEDPVELHKL 244
 QY 253 LRKSTFKNAKLYGPDVGOGRKRTAKMLKSPFKAGGEVIDSVTHHHYINGRTATREDFLN 312
 DB 245 LQKSAFQNAKLYGPDVGOGRKRTAKMLKSPFKAGGEVIDSVTHHHYINGRTATREDFLS 304
 QY 313 PDVLDIFISSVQKVFQVVESTRPGKRWLGETSSAYGAGAPLSDTFAAGFMWLDKLGIS 372
 DB 305 SDVLDIFILSYQKILKVTKEITPGKRWLGETSSAYGAGAPLSDTFAAGFMWLDKLGIS 364
 QY 373 ARMGIEVVRQVFFGAGNYHLDVENFPLPDYWSLFPKLVGTGKVLMAVYQSKRRKLR 432
 DB 365 AQMGIEVVRQVFFGAGNYHLDVENFPLPDYWSLFPKLVGTGKVLMAVYQSKRRKLR 424
 QY 433 VYLHCTNDNPRYKSGDILLVAINLHNTKYRLPYFPNSKNQVQKYLRLPGPHGLSKS 492
 DB 425 VYLHCTNVYHPRYQSGDILLVAINLHNTKYRLPYFPNSKNQVQKYLRLPGPHGLSKS 484
 QY 493 VOLNGILTKMVDQTLPLMEKPLRPGSSGLPAPSYSPFVIRNAKVACI 543
 DB 485 VOLNGILTKMVDQTLPLMEKPLRPGSSGLPAPSYSPFVIRNAKVACI 535

RESULT 5
 06Y6Z1 PRELIMINARY; PRT; 535 AA.
 AC 06Y6Z1;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Heparanase.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22841152; Pubmed=12837765; DOI=10.1074/jbc.M300925200;
 RA Gong F., Jench P., Galvis M.L.E., Vlodeavsky I., Horner A., Lindahl U.,
 RA Li J.-P.,
 RT "Processing of macromolecular heparin by heparanase."
 RU J. Biol. Chem. 278:35152-35158 (2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Li J.-P., Gong F., Lindahl U.;
 RU Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY151051; AAN41636.1; -
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); TAS.
 DR InterPro; IPR005199; Glyco_hydro_79N.
 DR Pfam; PF03662; Glyco_hydro_79n; 1.
 DR SEQUENCE 535 AA; 59992 MW; 3748AB3795C718A CRC64;
 SQ
 Query Match 75.3%; Score 2140; DB 2; Length 535;
 Best local Similarity 76.6%; Pred. No. 5e-152;
 Matches 407; Conservative 50; Mismatches 74; Indels 0; Gaps 0;
 QY 13 LMLLLGPIGLSPGALPRPAQADVDVDFDFTQEPHLIVSPFSLVTIDANLATDPRFL 72
 DB 5 LILMLMGPIGLALAGAPAGTAPTDVDFEFTYKRLRSVSPFSLITIDASTADPRFL 64
 QY 73 ILLGPKRLTARGLSPAYIRFGTKTDFLIPDKKESTFEERSYVQSQVNOIDCKYGS1 132
 DB 65 TFLGSPRLALARGSPAYIRFGTKTDFLIPDKKESTFEERSYVQSQVNOIDCKRBPV 124
 QY 133 PPVBEKRLRLEWVYQEOILLREHYOKFKFNSTYSRSVDVLYTFANCGSLDIFGINALL 192
 DB 125 SAAVLRKLVQWEPFQELLRLREYQKFKFNSTYSRSVDVLYTFANCGSLDIFGINALL 184
 QY 193 RTADLQNNSSNAQLLDYCSSKGNISWELGNEPNSFLKKAIDIFINGSQIGEDYIOLHKL 252
 DB 185 RTPDLRNNSSNAQLLDYCSSKGNISWELGNEPNSFWKKAHLLIDGLQIGEDPVELHKL 244
 QY 253 LRKSTFKNAKLYGPDVGOGRKRTAKMLKSPFKAGGEVIDSVTHHHYINGRTATREDFLN 312
 DB 245 LQKSAFQNAKLYGPDVGOGRKRTAKMLKSPFKAGGEVIDSVTHHHYINGRTATREDFLS 304
 QY 313 PDVLDIFISSVQKVFQVVESTRPGKRWLGETSSAYGAGAPLSDTFAAGFMWLDKLGIS 372
 DB 305 SDVLDIFILSYQKILKVTKEITPGKRWLGETSSAYGAGAPLSDTFAAGFMWLDKLGIS 364
 QY 373 ARMGIEVVRQVFFGAGNYHLDVENFPLPDYWSLFPKLVGTGKVLMAVYQSKRRKLR 432
 DB 365 AQMGIEVVRQVFFGAGNYHLDVENFPLPDYWSLFPKLVGTGKVLMAVYQSKRRKLR 424
 QY 433 VYLHCTNDNPRYKSGDILLVAINLHNTKYRLPYFPNSKNQVQKYLRLPGPHGLSKS 492
 DB 425 VYLHCTNVYHPRYQSGDILLVAINLHNTKYRLPYFPNSKNQVQKYLRLPGPHGLSKS 484
 QY 493 VOLNGILTKMVDQTLPLMEKPLRPGSSGLPAPSYSPFVIRNAKVACI 543
 DB 485 VOLNGILTKMVDQTLPLMEKPLRPGSSGLPAPSYSPFVIRNAKVACI 535

RESULT 6
 07IRP1 PRELIMINARY; PRT; 536 AA.
 AC 07IRP1;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Heparanase.
 GN Name=Hepar;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

RP SEQUENCE FROM N.A.
RA Hulet M.D., Wang J., Hornby J.R., Freeman C., Pagler E., McHenry J.,
RA Parish C.R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF359508; AAQ15189.1; -
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 536 AA; 60479 MW; C434E04CF536EAD CRC64;

Query Match 75.1%; Score 2135; DB 2; Length 536;
Best Local Similarity 76.1%; Pred. No. 1.2e-151;
Matches 407; Conservative 50; Mismatches 78; Indels 0; Gaps 0;

QY LPPPLMLLLGLPLSGALPRPAQADVDLDFPFQEPHLVSPSLSTIANLATD 68
DB 2 LRPPLLMWGRGLMGTGTGTAFTKDVVDLEFYTKLFQSVSPSLSTIDASTLATD 61
QY 69 PRFLILGSPRLRLARGSPAYLRFGGTKTDFLIPDKESTFEERSYMOSONODICK 128
DB 62 PRFLIFGSPRLRLARGSPAYLRFGGTKTDFLIPDKESTFEERSYMOSONODICK 121
QY 129 YGSIIPDVEEKLRLMPYQEQLLREHYQKKFKNSTYSSSDVLYTFANCSGLDLIFGL 188
DB 122 SERVSADVLRLQWEMPFQELLLREYQREKFNSTYSSSDVLYTFANCSGLDLIFGL 181
QY 189 NALRTADLQWSSNAQILLDYCSSKGYNISWELGNEPNSFLKXADIFINSGQGEDVYE 248
DB 182 NALRTADLQWSSNAQILLDYCSSKGYNISWELGNEPNSFLKXADIFINSGQGEDVYE 241
QY 249 LHKLRKSTFPKNAKLYGPDVGQPRKRTAKMLKSLFKAGEVIDSYTMHHYLLNGRTATRE 308
DB 242 LHKLRKSTFPKNAKLYGPDVGQPRKRTAKMLKSLFKAGEVIDSYTMHHYLLNGRTATRE 301
QY 309 DFLNDVDLFISSVQKVFQVVESTRPGKRWLGETSSAYGGAPLSDTPAAGFMWLDK 368
DB 302 DFLNDVDLFISSVQKVFQVVESTRPGKRWLGETSSAYGGAPLSDTPAAGFMWLDK 361
QY 369 LGLSARMGIEVVMQVFFGAGNYHLVDENFPLDYMLSLFKLVGTRKYLMAVSQSKR 428
DB 362 LGLSARMGIEVVMQVFFGAGNYHLVDENFPLDYMLSLFKLVGTRKYLMAVSQSKR 421
QY 429 RKLRYLHCTNDNRYKEGDLTYAHLNHYTKYLRPYPSNKQVDKYLRLPGPGGL 488
DB 422 SKLRVYLHCTNVYHRYREGDLTYAHLNHYTKYLRPYPSNKQVDKYLRLPGPGGL 481
QY 489 LSKSVQNLGLTKLVVDQTLPLMEKPLRPGSSSLGLPAFYSFVIRNAKVAACI 543
DB 482 LSKSVQNLGLTKLVVDQTLPLMEKPLRPGSSSLGLPAFYSFVIRNAKVAACI 536

RESULT 7
Q9QZF8 PRELIMINARY; PRT; 536 AA.
AC Q9QZF8; 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hepatanae.
GN Name=Hep;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=22194309; PubMed=12077130; DOI=10.1074/jbc.M203282200;
RT Podmya-Inoue K.A., Yokoe H., Sakaguchi K., Ikuta M., Yanagishita M.;
RT "Characterization of hepatanae from a rat parathyroid cell line.";
RL J. Biol. Chem. 277:32455-32465(2002).
RN (2)
RP SEQUENCE FROM N.A.
RA Podmya K.A., Yokoe H., Sakaguchi K., Ikuta M., Yanagishita M.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF184967; AAF04563.1; -
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 536 AA; 60568 MW; 6208B1FDEE28421 CRC64;

Query Match 74.7%; Score 2123; DB 2; Length 536;
Best Local Similarity 75.7%; Pred. No. 9.5e-151;
Matches 405; Conservative 51; Mismatches 79; Indels 0; Gaps 0;

QY 9 LPPPLMLLLGLPLSGALPRPAQADVDLDFPFQEPHLVSPSLSTIANLATD 68
DB 2 LRPPLLMWGRGLMGTGTGTAFTKDVVDLEFYTKLFQSVSPSLSTIDASTLATD 61
QY 69 PRFLILGSPRLRLARGSPAYLRFGGTKTDFLIPDKESTFEERSYMOSONODICK 128
DB 62 PRFLIFGSPRLRLARGSPAYLRFGGTKTDFLIPDKESTFEERSYMOSONODICK 121
QY 129 YGSIIPDVEEKLRLMPYQEQLLREHYQKKFKNSTYSSSDVLYTFANCSGLDLIFGL 188
DB 122 SERVSADVLRLQWEMPFQELLLREYQREKFNSTYSSSDVLYTFANCSGLDLIFGL 181
QY 189 NALRTADLQWSSNAQILLDYCSSKGYNISWELGNEPNSFLKXADIFINSGQGEDVYE 248
DB 182 NALRTADLQWSSNAQILLDYCSSKGYNISWELGNEPNSFLKXADIFINSGQGEDVYE 241
QY 249 LHKLRKSTFPKNAKLYGPDVGQPRKRTAKMLKSLFKAGEVIDSYTMHHYLLNGRTATRE 308
DB 242 LHKLRKSTFPKNAKLYGPDVGQPRKRTAKMLKSLFKAGEVIDSYTMHHYLLNGRTATRE 301
QY 309 DFLNDVDLFISSVQKVFQVVESTRPGKRWLGETSSAYGGAPLSDTPAAGFMWLDK 368
DB 302 DFLNDVDLFISSVQKVFQVVESTRPGKRWLGETSSAYGGAPLSDTPAAGFMWLDK 361
QY 369 LGLSARMGIEVVMQVFFGAGNYHLVDENFPLDYMLSLFKLVGTRKYLMAVSQSKR 428
DB 362 LGLSARMGIEVVMQVFFGAGNYHLVDENFPLDYMLSLFKLVGTRKYLMAVSQSKR 421
QY 429 RKLRYLHCTNDNRYKEGDLTYAHLNHYTKYLRPYPSNKQVDKYLRLPGPGGL 488
DB 422 SKLRVYLHCTNVYHRYREGDLTYAHLNHYTKYLRPYPSNKQVDKYLRLPGPGGL 481
QY 489 LSKSVQNLGLTKLVVDQTLPLMEKPLRPGSSSLGLPAFYSFVIRNAKVAACI 543
DB 482 LSKSVQNLGLTKLVVDQTLPLMEKPLRPGSSSLGLPAFYSFVIRNAKVAACI 536

RESULT 8
Q9QYK5 PRELIMINARY; PRT; 523 AA.
AC Q9QYK5; 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hepatanae.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=21369599; PubMed=11387326; DOI=10.1074/jbc.M102462200;
RA Goldsmith O., Zcharia E., Alingorn H., Guarte-Rangini Z., Azmon R.,
RA Michael I., Becker I., Mitrani E., Vlodavsky I.;
RT "Expression pattern and secretion of human and chicken heparanase are
RT determined by their signal peptide sequence.";
RL J. Biol. Chem. 276:29178-29187(2001).
DR EMBL; AY037007; AAK82648.1; -
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 523 AA; 58386 MW; 8EB0B7B18C9BF81 CRC64;

Query Match 57.9%; Score 1645.5; DB 2; Length 523;
Best Local Similarity 60.2%; Pred. No. 6.8e-115;

Qy	13	IMLLIGRGPALPPRAQADVDVLDFFTEPHLTVSPFLSTVIDANLATDPRFL	
Dd	2	LVLTLVLTLAAPP-----BRTAFLQGLGREPIGAVSPAFSLTIDASLADPRFV	
Qy	73	ILUGSPKLTTLTAGLSPAYLRFPGGKIDFLIPDKKSTFEENSQVNOVODICKYSI	132
Dd	53	ALLRHPKHLTLASGLSPGLRFGSTIDFLFNKNDSTWEKVLSEFGA-KDVEAMPS	111
Qy	133	PDVBEKRLREPVYEOULLREHYOKFKQKSTYSSRSVDVLYTFANCGLDIPGLMNL	192
Dd	112	FAVVKKLLTQMPLOEKLTLAHSWKGKHTTTRSTLDLHTPASSGGRFLVEGNALL	171
Qy	193	RTADLQWNSNAOLLDDYCSKGNISWELGNENPNSFLKKAIDIFINGQLGEDIYQLHKL	252
Dd	172	RRAGIQWDSNAQGLDLYCAQGRGNISWELGNENPNSFRKKSIGCIDGQLRDFVHROL	231
Qy	253	L-RKSTFENALYPPDVQGRPKTKALMSFLKAGGEVIDSVYTHHYLYNGRTATRPDL	311
Dd	232	LSQHPYLRHMLVGLDVGQPRKTHOHLRSFPMKSGKALDSVTMHYHYVNRKSTRDDL	291
Qy	312	NPVDVLDIFISSVOKVFEQVNSTPFGKMWLGENSSVGGGAPLSDTPAAGFMWLDYGL	371
Dd	292	SPEVLDLFATAYADHVGLVETATPGKKVWLGETSATYGGAPQLSNTRYVAGFMWLDYGL	351
Qy	372	SARVGIEVNRQVYFRGAGNYHVDENFDLPDYMLSLFKLVGTIKYLMASVQSKRRKL	431
Dd	352	AARGIDIVNRQVSPAGSGLHVDAGFKLPPYMLSLTKYRLVGRVQLQSVGQADARR	411
Qy	432	RVYLHCTNTNDPRYKGGDLTYLAIMLHNTYKTLRPYFNSKQVDKYLAPLCPHGLSK	491
Dd	412	RVYLHCTNPBPRYRGDVTLPALNLSVTQSLQLPKQMSKVQDYLLPHKDSILSR	471
Qy	492	SVQNLGLTKMVDQDTLPFLMEKLPDPSSIGLPAFSYSPFYRNAAVACI	543
Dd	472	EVQNLRLQWVDDETLPALHEMALPESITGLPFAFYGFVIRNAAVACI	523

RESULT 9

09HB37

ID	Q9HB37	PRELIMINARY:	PRT:	592 AA.
AC	Q9HB37			
DT	01-MAR-2001 (Tremblrel. 16, Created)			
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)			
DE	01-JUN-2003 (Tremblrel. 24, Last annotation update)			
OS	Heparanase-like protein HPA2C.			
OC	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteria; Primates; Carnivora; Homnidae; Homo.			
ON	NCBI_TaxID=9606;			
OX				
RP	SEQUENCE FROM N.A.			
RA	McKenzie E.A., Tyson K., Stamps A.,			
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF282887; AAC23423.1; -			
DR	GO; GO:0005622; C:intracellular; TAS.			
DR	GO; GO:0030305; F:heparanase activity; TAS.			
DR	InterPro; IPR005199; Glyco_hydro_79N.			
DR	Pfam; PF03662; Glyco_hydro_79n.1.			
DR	SEQUENCE 592 AA; 66580 MW; 95CG344AD9A74258B CRC64;			
QO				

[illegible]

RESULT 10			
ID	Q8BWMQ2	PRELIMINARY;	PRT; 592 AA.
AC	Q8BWMQ2;		
DT	01-MAR-2002 (TrEMBLrel. 20, Created)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	Heparanase 2.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1] _		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Prostate;		
RA	Legoux P., Legoux R., O'Brien D., Salome M.;		
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Prostate;		
RA	Peessgaie Safontas B, J, O.P.S.;		
RL	Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AJ299719, CAC92491.1, -		
DR	Genew; HGNC:18374, HPSE2.		
DR	Pfam; PF03662; Glyco Hydrol 79n; 1.		
SEQUENCE	592 AA; 66520 MW; 9478841FEACD55AR CROCA.		

Query Match	40.3%	Score 1146.5;	DB 2;	Length 592;
Best Local Similarity	43.4%;	Pred. No. 2.5e-77;		
Matches 249; Conservative	82;	Mismatches 190;	Indels 53;	Gaps 9

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Qy 20 PLGLSPGAL-----PRPA-----QAQDVVDLDEFTQEPHLVSPS 55
    |||||
Db 18 PPACIAPGALYALALLHLHLSLSSQAGDRRLPVPDRAAGLKEKTLILDVSTKNPVRTVEN 77
    |||||
Qy 56 FLSTVIDANLATDPRFLILGSPKRLTARGLSPAYLRFGTKTDPLIF---DPKEST 111
    |||||
Db 78 FLSTQLDPSIIHD-CWLDPLSSKRLVTLARGLSPAFLEFGGKRTDPLQFONLRNPAKSRG 136
    |||||
Qy 112 FEEBRYSQVQVNOI-----CKYGSIPPDVEEKLRLRMPYEQQL-LIREHQK 158
    |||||
Db 137 GPGPDYILKNYEDDLYRSDVADLKQKCKLIAQ-HPDVYLELOREKAAQWHLLEQPSN 195
    |||||
Qy 159 KFKNSTYRSADVLYTFPANCGLDLIFGLNALRTADLQWNSNAQLLDYCSSKGYNI 218
    |||||
Db 196 TYSNLIIFARSLDKLYNSADCSGLHIFALNALRRPNNSWSSSALSLTKXSARKKXNI 255
    |||||
Qy 219 SWEIENEPNSFLKKADIFINGSQIGEDYIQLHKLIRK-STFKNAKLYGPDVGQPPRKTA 277
    |||||
Db 256 SWEIENEPNNYRTMGRAVNGSQIGEDYIQLKSLQPIRIYSRAQLYGNIGRPKNVYA 315
    |||||
Qy 278 MLKSLFKAGGEVIDSVTHHHYVINGRTATREDPLNDVDLFISSVQKVFQVVESTRPCK 337
    |||||
Db 316 LLDGFKVAAGSTVDVATWQHCYIDGRVVKVMDPLKTRLDLTDLSQIRIKIQKVNNTYTPGK 375
    |||||
Qy 338 KVMIGETSSAYGGAPLSDTFAAGFMWLDKGLSARWGI EYVMROVFEGAGNYHLYDEN 397
    |||||
Db 376 KIMLEGVTTTSAGCTNNLSDSYAAGFLMNTLGMLANQIDIVYIHSFPHGYNHLVDON 435
    |||||
Qy 398 PDPPLDYMLSLFKLVGTRKVLMAVSQSKRR-----KLRYVLYHCTNTDNPYKRG 448
    |||||
Db 436 FNPPLDYMLSLFKLVGTRKVLMAVSQSKRR-----KLRYVLYHCTNTDNPYKRG 495
    |||||
Qy 449 DLTVAIYLNHNTKYLRLPYPSNKOVDKYLRLPGPHGLSKSVQNLGTLTKMDDDTL 508
    |||||
Db 496 SITFLIINLHRSRKIKLAGTLRDLKVHQYLLQPYQGBELSKSVQNLGTLTKMDDDTL 555
    |||||
Qy 509 PPLMEKPLRPGSSGLPAPFSYFPYIRNAKVAAC 542
    |||||
Db 556 PELKRPPLRAGRTLYIPPTWGMFVYKVNALAC 589
    |||||

RESULT 11
Q8MWQ1 PRELIMINARY; PRT; 548 AA.
ID 08MWQ1 AC Q8MWQ1.
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Heparanase 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Legoux P., Legoux R., O'Brien D., Salome M.;
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Peasegue Safontas B J O P S.;
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ299720; CAC82492.1; -.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 548 AA; 61771 MW; B8986303FC73A60A CRC64;

Query Match 35.7%; Score 1015.5; DB 2; Length 548;
Best Local Similarity 41.8%; Pred. No. 1.6e-67;
Matches 224; Conservative 79; Mismatches 180; Indels 53; Gaps 9;

Qy 8 ALPPLMLLLGLPLSPGAL-----PRPA-----QAQDVVDLDF 43
    |||||

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Db 6 AFPEAMLSNSNRPPACIAPGALYALALLHLHLSLSSQAGDRRLPVPDRAAGLKEKTLILDV 65
    |||||
Qy 44 FTQEPHLVSPSFLSTVIDANLATDPRFLILGSPKRLTARGLSPAYLRFGTKTDPLI 103
    |||||
Db 66 STKNPVRTVENNPSFLQDPSIIHD-CWLDPLSSKRLVTLARGLSPAFLEFGGKRTDPLQ 124
    |||||
Qy 104 F-----DPKESTFEEBRYSQVQVNOI-----CKYGSIPPDVEEKLRLRMPYEQ 147
    |||||
Db 125 FQNLNRPAPKSGGCGPDYILKNYEDDLYRSDVADLKQKCKLIAQ-HPDVYLELOREKAAQ 183
    |||||
Qy 148 EQL-LIREHQKFKRKNSTYRSADVLYTFPANCGLDLIFGLNALRTADLQWNSNAQL 206
    |||||
Db 184 MHLVLYLKEQFQNTSNLIIFARSLDKLYNSADCSGLHIFALNALRRPNNSWSSSALS 243
    |||||
Qy 207 LLDYCSSKGYNISWEIENEPNSFLKKADIFINGSQIGEDYIQLHKLIRK-STFKNAKLYG 265
    |||||
Db 244 LKTSASARKYNI SWEIENEPNNYRTMGRAVNGSQIGEDYIQLKSLQPIRIYSRAQLYGN 303
    |||||
Qy 266 PIVQPPRRKTAQMLKSLFKAGGEVIDSVTHHHYVINGRTATREDPLNDVDLFISSVQK 325
    |||||
Db 304 PNIGRPKNVIALLDGFKVAAGSTVDVATWQHCYIDGRVVKVMDPLKTRLDLTDLSQIRK 363
    |||||
Qy 326 VFQVESTRPCKKVMIGETSSAYGGAPLSDTFAAGFMWLDKGLSARWGI EYVMROVF 385
    |||||
Db 364 IQKVNNTYTPGKTIWLEGVTTTSAGCTNNLSDSYAAGFLMNTLGMLANQIDIVYIHSF 423
    |||||
Qy 386 FGAGNYHLYDENPDPRLPYMLSLFKLVGTRKVLMAVSQSKRR-----KLRYVLYH 436
    |||||
Db 424 FDHGYNHLVDONFNPPLDYMLSLFKLVGTRKVLMAVSQSKRR-----KLRYVLYH 483
    |||||
Qy 437 CTNTDNPYKRGDITLVAIYLNHNTKYLRLPYPSNKOVDKYLRLPGPHGLSKSV 492
    |||||
Db 484 CTNNHNNYVAGSITFLIINLHRSRKIKLAGTLRDLKVHQYLLQPYQGBELSKSV 539
    |||||

RESULT 12
Q9HB38 PRELIMINARY; PRT; 534 AA.
ID 09HB38 AC Q9HB38.
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Heparanase-like protein HPA2b.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20483645; PubMed=11027606; DOI=10.1006/dbrc.2000.3586;
RA McKenzie E., Tyson K., Stamps A., Smith P., Turner P., Barry R.,
RA Hitcock M., Patel S., Barry E., Stuberfield C., Terrett J., Page M.;
RT "Cloning and expression profiling of Hpa2, a novel mammalian
RT heparanase family member.";
RL Biochem. Biophys. Res. Commun. 276:1170-1177 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA McKenzie E.A., Tyson K., Stamps A.;
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF282886; AAC33422.1; -.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 534 AA; 60063 MW; C3DB5900CB338C4 CRC64;

Query Match 33.0%; Score 936.5; DB 2; Length 534;
Best Local Similarity 37.8%; Pred. No. 1.3e-61;
Matches 217; Conservative 78; Mismatches 168; Indels 111; Gaps 12;

Qy 20 PLGLSPGAL-----PRPA-----QAQDVVDLDEFTQEPHLVSPS 55
    |||||
Db 18 PPACIAPGALYALALLHLHLSLSSQAGDRRLPVPDRAAGLKEKTLILDVSTKNPVRTVEN 77
    |||||
Qy 56 FLSTVIDANLATDPRFLILGSPKRLTARGLSPAYLRFGTKTDPLIF---DPKEST 111
    |||||

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Db 78 FLSTLDPSIIHD-GWLDFFLSKRLVTARGLSPAFLRFGKRTDFOQLNRNPAKSRG 136
QY 112 FEERSYMSQVNODI-----CKYGIIPDVEEKLRLWPYQOL-LLREHYOK 158
Db 137 GPGDYLYKNEYEDIVRSVALDKOKGCKIAQ-HPDVMLELQREKAAQMHVLVLLKEGF-- 133
QY 159 KFKSTYSRSSVDVLYTFPANCGLDLYFGNALRLRTADLQWNSNAQLLLDYCSSKGYNI 218
Db 194 ---SNVYS-----NLII----- 202
QY 219 SWEIGNEPNSFLKADIFINGSQIGEDYIQLHKLK-STEKNAKLYGPDVQPRKRTAK 277
Db 203 -----TEPNNYRTMNGRAVNSQIGKDYIQLKSLQIRIYSRASILGPNIGPRKQVIA 257
QY 278 MLKSLFKAAGEVIDSYTHHYYLNGRATREDFLNPVDLFISSVQKFOVVESTRPEK 337
Db 258 ILDSFMKVASGYDAVYWHQCHYIDGRVYKVMDFLKRLLDPTLSDOIRKIQKVNTVTPPK 317
QY 338 KWIIGETSSAYGQAPLLSDTFAAGFMWLDKGLSARMGIEVYMRQVFGAGNYHLVDEN 397
Db 318 KIMLEGVVTTSAGGTNNLSDSAAGFLMNTLGLANOGIDVYIRHSFPDHGYNHLVDON 377
QY 398 FDPFLPYWLSLTKPKLVGTQVLMASVQSGRR-----KLRYLHCTNTDNPRYKRG 448
Db 378 FNFLPYWLSLTKPKLVGTQVLMASVQSGRR-----KLRYLHCTNTDNPRYKRG 437
QY 449 DLTLYAINHNVTXYLRLPYPSNKOVDXYLLRPLGPHGLSKSVOLNGTLKMYDDOTL 508
Db 438 SYLFPYINLHRSRKKIKLAGTRLDKLVHGYLLQPYQGBELKSKSVOLNGQPLVMWDDGTL 497
QY 509 PPLMEKLRPGSLGIFAFSYSPFYIRNAKVAAC 542
Db 498 PELKRPRLAGRTLVLPVYTMGFVVKVNNALAC 531

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RESULT 13

Q9HB39

ID 09HB39 PRELIMINARY; PRT; 480 AA.

```

AC 09HB39;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Heparamase-like protein HPA2a.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20483645; PubMed=11027606; DOI=10.1006/jbrc.2000.3586;
RA McKenzie E., Tyson K., Stamps A., Smith P., Turner P., Barry K.,
RA Hitcock M., Patel S., Barry E., Stuberfield C., Terrett J., Page M.;
RT "Cloning and expression profiling of Hpa2, a novel mammalian
RT heparanase family member."
RL Biochem. Biophys. Res. Commun. 276:1170-1177(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA McKenzie E.A., Tyson K., Stamps A.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282885; AAC23421.1; -.
DR JCT506; JCT506.
DR InterPro: IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 480 AA; 53900 MW; F75F89F67AC1PF83 CRC64;

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Query Match

Best Local Similarity 31.6%; Score 897.5; DB 2; Length 480;
Matches 202; Conservative 74; Mismatches 146; Indels 139; Gaps 9;

```

QY 20 PLGLSPGAI-----PRPA-----OAOVVDVDFPTQSPHLVPS 55
Db 18 PRACLAPGALYALTLHLTSLSSQAGRRRLPVDRAAGLKEKTLILLDVTYKQVARTVEN 77

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QY 56 FLSTVTDANLMDPRFLILSSPKLRTARGLSPAFLRFGKRTDPIF-----DPKEST 111
Db 78 FLSTLDPSIIHD-GWLDFFLSKRLVTARGLSPAFLRFGKRTDFOQLNRNPAKSR- 135
QY 112 FEERSYMSQVNODICKYGIIPDVEEKLRLWPYQOLLLREHYOKKFKNSTYSRSSVD 171
Db 136 -----GGRGP-----YLLKVE----- 148
QY 172 VLYTFPANCGLDLYFGNALRLRTADLQWNSNAQLLLDYCSSKGYNI SWEIGNEPNSFLK 231
Db 149 -----DEPNNYRT 156
QY 232 KADIFINGSQIGEDYIQLHKLK-STEKNAKLYGPDVQPRKRTAKMLKSLFKAAGEVI 290
Db 157 MEGRAVNSQIGKDYIQLKSLQIRIYSRASILGPNIGPRKQVIALLDGFMKVASGYV 216
QY 291 DSYTHHYYLNGRATREDFLNPVDLFISSVQKFOVVESTRPEKQWLGETSAYG 350
Db 217 DAVYWHQCHYIDGRVYKVMDFLKRLLDPTLSDOIRKIQKVNTVTPPKKIMLEGVVTTSAG 276
QY 351 GAPLSDTFAAGFMWLDKGLSARMGIEVYMRQVFGAGNYHLVDENPPLPDYWLSTLF 410
Db 277 GTNNLSDSAAGFLMNTLGLANOGIDVYIRHSFPDHGYNHLVDONFNPLDYWLSLILY 336
QY 411 KKLVTQVLMASVQSGRR-----KLRYLHCTNTDNPRYKRGDLTYAINLHNVT 461
Db 337 KRLIGPVLAHVAGLQKRPGRVIRDKRLRYAHCTNHNHNHYRGSITLPIINLHRS 396
QY 462 KYLRLPYPSNKOVDXYLLRPLGPHGLSKSVOLNGTLKMYDDOTL PPLMEKLRPGSS 521
Db 397 KKLKLAGTRLDKLVHGYLLQPYQGBELKSKSVOLNGQPLVMWDDGTLPELKRPRLAGRT 456
QY 522 LGLPASFYSPFYIRNAKVAAC 542
Db 457 LVLPVYTMGFVVKVNNALAC 477

```

RESULT 14

O8T108

ID O8T108 PRELIMINARY; PRT; 515 AA.

```

AC O8T108;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Heparamase-like protein.
GN Name=Bmbpa; (Silk moth).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxId=7091;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=p50; TISSUE=Posterior silkland;
RA Koike Y., Mita K., Suzuki M.G., Maeda S., Abe H., Osoegawa K.,
RA deJong P.J., Shimada T.;
RT "Genomic sequence of a 320-kb segment of the Z chromosome of Bombyx
RT mori containing a ketin ortholog."
RL Mol. Genet. Genomics 269:137-149(2003).
DR EMBL; AB079860; BAB85191.1; -.
DR EMBL; AB090307; BAC10612.1; -.
DR InterPro: IPR005199; Glyco_hydro_79N.
DR Pfam; PF03662; Glyco_hydro_79n; 1.
SQ SEQUENCE 515 AA; 59769 MW; FB8100AB6EDDADB CRC64;

```

Query Match

Best Local Similarity 24.5%; Score 696; DB 2; Length 515;
Matches 183; Conservative 83; Mismatches 182; Indels 74; Gaps 18;

```

QY 46 QEPHLVSPFSFSLVTDANLMDPRFLILSSPKLRTARGLSPAFLRFGKRTDPIFD 105
Db 42 QEDIKLSBDFLFGID-TIETENYRINYSDTRLRELAALSPARLRLRGITMSRLIF- 99

```

QY 106 PKSESTFEERSYQWQVNOQDICKYSGISPPDVEKLEMPYQBOQLLREHYOKKFKNSTY 165
DB 100 -SKENI-----PISCHNCSTYKSPKSLCQ--LIEKPC-----KHKKKLPFFIM 140
QY 166 SRSSVDLYTTFANCSCGLDLIFGLNALRTADLQWNSNAQLLDYCCKSGYNI SWELGNE 225
DB 141 TGNENWQINDFCRKTNLKLFLSLNMLRD-NHGMNEKARLELIEPSKHQVADIDQLGNE 199
QY 226 PMSFLKADIFINGSQLEDYIQLHKLKRSKTFKAKLYGPVGP---RRTATMLKSF 282
DB 200 PMSFHVNESVTPOILAKDPEKRLKLNHNGYRSLVGPDTTRQPHRPECLKYLIEF 259
QY 283 LKAGEVIDSVTHHYLYNGRATREDFLNPDVLIFISSVQKQVVESTPEKKV--W 340
DB 260 LANGSHYINWRSKHQYILNSTRKAKLEDFFNPEPTPLL--RQIETMQNTKYYNIEMW 316
QY 341 LGETSSAYGGAPLLSDTFAAGFMWLDKLGLSARNGIEVNRQVFFGAGNYHLDENPD 400
DB 317 LSETSSYGGAGPLSNTYAGSPMLWIDKLGLSAKYNI STVIRQSPFG--GYSLVDENLKP 375
QY 401 LPDYLSLFLFKLVGTKYLMAVQSGSKRKLRYVLTCTNDNPRYKE--GDLTYAIN-- 456
DB 376 LPDMWISVLYKKLVGNKYL--QVQNCGRFQRLYHCTNR--KYTNDTSAVTLXGVNDE 430
QY 457 -----LHN-----VTKYRLPYPSNKOVDKYLRLPGLPHGLSKSVOLNGLTL 500
DB 431 MAKAPFLNGTALHGDLDLIHEYI-ISAPSNRK-----SKTIILNGMPL 474
QY 501 KMWDDQTLPLMEKPLRPSSSLGLPAFYSFPFVINNAKVAAC 542
DB 475 YY--BSNLHNLRLPNHRYGRYVSLPPLPSIGFWVIKTSITVC 514

RESULT 15

Q9SDA1 PRELIMINARY; PRT; 521 AA.
ID Q9SDA1 AC Q9SDA1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein F13G24.30.
GN Name=F13G24.30;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosidia II; Brassicales; Brassicaceae; Arabidopsia.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Beyer M., Van Der Schueren J., Chuang Y.J., Voet M., Robben J.,
RA Volekær G., Bancroft I., Mewes H.W., Lemcke K., Mayer K.F.X.,
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
DB EMBL; AL133421; CAB62595.1; --
DB PIR; T45608; T45608.
DR InterPro; IPR005199; Glyco_hydro_79N.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF03662; Glyco_hydro_79n_1.
DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 521 AA; 57831 MW; 07D8664AAB305CC2 CRC64;

Query Match 14.6%; Score 416; DB 2; Length 521;
Best Local Similarity 29.2%; Pred. No. 1.6e-22;
Matches 154; Conservative 68; Mismatches 184; Indels 122; Gaps 24;

QY 75 LGSPLKRLTLANGSLPAYRFGSTKTDPLIFDPKKESTFEERSYQWQVNOQDICKYSGISLP 134
DB 55 LTRPLTLRAIKAFKFLIRIGSLQDOVYIVDGNLKT-----PCR----- 94

QY 135 DVEEKLRLMEPYQOQLLREHYOKKFKNS---TYSRSSV-----DLYTFANCSCGLDLIF 186
DB 95 -----PFQCK-----NSGLFGSSKGLHKKRDELNSFLTAGAVTFF 132
QY 187 GLNALRLRTADLQ-----WNSSNAQLLDYCCKSGYNI SWELGNEPNSFLKADIFIN 238
DB 133 GLNALRGRHKLRGKAMGAGMDHINTQDPLANTYKGVYIDMERGNELSG--SGVGASVS 190
QY 239 GSQLEDYIQLHKLKRSKTFKAKLYGPVGP-----RRTATMLKSF LKAGEVIDSV 293
DB 191 AELYGKDLIVLKDVYINK--VYNSWMLHKEILVAPGFGYEQQWYTKLLET--SGBSVDVV 246
QY 294 TWHHYLYNGRT--ATREDFLNPDVLIFISSVQKVF-----QVVESTPEKKKWLGETSSA 347
DB 247 TTHIYNLGSNDPPLVKKIMPS-----YLSQVSKTFKQVNTIQEHGMAWSPWGESGGA 302
QY 348 YGGAPPLSDTFAAGFMWLDKLGLSARNGIEVNRQVFFGAGNYHLDENPDLPDYWL 406
DB 303 YNSGGRHVSDTFIDSFMYLDQLGMSARHNTKYVCGQLVIG--GFYGLLEKGTFFVPRPDYYS 361
QY 407 SLFLKLVGTKYLMAVQSGSKRKLRYVLTCTNDNPRYKEGDLTYAINLHNTKYL-- 464
DB 362 ALLMHRMLMGKGLAVVQTDGPP--QLRYVAHCSK-----GRAGYTLILINLSNOSDFTVS 413
QY 465 -----RLPYPS-----NKQVDKYLRLP-----LGPHG--LISKSYQL 495
DB 414 VSNGINVVLNANESRKKSILDTLKRPFWSWISKASDGYLNREETHLTPENGVLNSKTIWVL 473
QY 496 NGLTLKMWDDQTLPLMEKPLRP--GSLGLPAFYSFPFVINNAKVAAC 542
DB 474 NGSILKPTATGDIPSL--EPVLRSVNSPLNVLPLMSFVLNPNPASAC 520

Search completed: February 28, 2005, 06:08:39
Job time : 184 secs

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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: February 28, 2005, 05:52:45 ; Search time 172 Seconds
(without alignments)
1220.994 Million cell updates/sec

Title: US-10-786-149-2
Perfect score: 2842
Sequence: 1 MLRSKPAPEPMLLLGP.....LPAPSYSPFVIRNKAACI 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2842	100.0	543	2	AAV02345 A human h
2	2842	100.0	543	3	AAV57590 Human hep
3	2842	100.0	543	3	AAV08849 Amino aci
4	2842	100.0	543	3	AAV52990 Human hep
5	2842	100.0	543	4	AAV97635 Human hep
6	2842	100.0	543	5	ABV07813 Human hep
7	2842	100.0	543	7	ADG88800 Human hpa
8	2842	100.0	543	8	ADL16379 Human hep
9	2842	100.0	543	8	ADM48716 Human hpa
10	2842	100.0	592	2	AAV02346 A human h
11	2842	100.0	592	3	AAV08850 Amino aci
12	2842	100.0	592	7	ADG88804 Human SK-
13	2842	100.0	592	7	ADL16383 Human hep
14	2842	100.0	592	8	ADM48720 Human SK-
15	2838	99.9	543	2	AAV17082 Human hep
16	2838	99.9	543	4	AAV86206 Human hep
17	2838	99.9	543	7	ADD18950 Human dis
18	2838	99.9	543	8	ADK52086 Human ato
19	2838	99.9	543	8	ADM48759 Human hpa
20	2838	99.9	543	8	ADM05074 Antipsocti
21	2838	99.9	543	8	ADM04802 Antipsocti
22	2838	99.9	543	8	ADG80372 Heparinas
23	2838	99.9	543	8	ADH88210 Human pre
24	2838	99.9	543	8	ADP25079 PRO polyp
25	2838	99.9	588	2	AAV30124 A human p

26	2832	99.6	543	8	ADO63831 Human hep
27	2832	99.6	543	8	ADO63823 Human hep
28	2832	99.6	543	8	ADO63832 Human hep
29	2832	99.6	543	8	ADO63822 Human hep
30	2826	99.4	543	4	AAV88361 Human mem
31	2826	99.4	543	8	ADO63824 Human hep
32	2817	99.1	545	6	ABP56822 Human hep
33	2817	99.1	545	6	ADP16012 G-coupled
34	2817	99.1	545	8	ADL93951 Human G-c
35	2764	97.3	530	2	AAV34173 Human pre
36	2737	96.3	532	2	AAV17083 Seq ID No
37	2673.5	94.1	527	5	ABV07815 Chicken s
38	2673.5	94.1	527	7	ABW02018 Chimeric
39	2667.5	93.9	527	8	ADO63825 Chimeric
40	2667.5	93.9	527	8	ADO63826 Chimeric
41	2661.5	93.6	527	8	ADO63827 Chimeric
42	2146	75.5	535	3	AAV08851 A murine
43	2146	75.5	535	5	ABV07811 Mouse hep
44	2146	75.5	535	7	ADG88834 Mouse hpa
45	2146	75.5	535	8	ADL16413 Mouse hep

ALIGNMENTS

RESULT 1					
AAV02345	ADV02345	standard; protein, 543 AA.			
XX	XX	AAV02345;			
AC	AC	09-JUL-1999 (first entry)			
DT	DT				
XX	XX	A human heparanase protein.			
DE	DE				
XX	XX	Heparanase; hp; modulator; heparin-binding growth factor;			
KW	KW	cellular response; cytokine; cell interaction; plasma lipoprotein;			
KW	KW	cellular susceptibility; infection; disintegration;			
KW	KW	neurodegenerative plaque; wound healing; angiogenesis;			
KW	KW	atherosclerosis; inflammation; neurodegenerative disease; neutralise;			
KW	KW	plasma heparin; microvasculature; autoimmune lesion; renal failure.			
OS	OS	Homo sapiens.			
XX	XX				
PN	PN	W09911798-A1.			
PD	PD	11-MAR-1999.			
XX	XX				
PF	PF	31-AUG-1998; 98WO-US017954.			
XX	XX				
PR	PR	02-SEP-1997; 97US-00922170.			
PR	PR	02-JUL-1998; 98US-00109386.			
XX	XX				
PA	PA	(INSI-) INSIGHT STRATEGY & MARKETING LTD.			
PA	PA	(HADA-) HADASIT MEDICAL RES SERVICES & DEV.			
PA	PA	(FRIE/) FRIEDMAN M M.			
XX	XX				
PI	PI	Pecker I, Violdavsky I, Feinstein E;			
XX	XX				
DR	DR	WPI, 1999-302255/25.			
DR	DR	N-PSDB; AAX35648.			
XX	XX				
PT	PT	New human polynucleotide useful for treating angiogenesis, restenosis,			
PT	PT	and inflammation.			
XX	XX				
PS	PS	Claim 6; Fig 1; 63pp; English.			
XX	XX				
CC	CC	The specification describes a polypeptide having heparanase (hp)			
CC	CC	activity. The recombinant protein is used as a modulator of heparin-			
CC	CC	binding growth factors, cellular responses to heparin-binding growth			
CC	CC	factors and cytokines, cell interaction with plasma lipoproteins,			
CC	CC	cellular susceptibility to viral, protozoal and bacterial infections or			
CC	CC	disintegration of neurodegenerative plaques. Heparanase may be useful for			

CC conditions such as wound healing, angiogenesis, restenosis,
 CC atherosclerosis, inflammation, neurodegenerative diseases, and viral
 CC infections. Mammalian heparanase can be used to neutralize plasma
 CC heparin, and anti-heparanase antibodies may be applied for
 CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and
 CC renal failure in biopsy specimens, plasma samples, and body fluids. The
 CC present sequence represents human heparanase
 XX
 SQ Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 2; Length 543;
 Best Local Similarity 100.0%; Pred. No. 2.5e-273;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MLRSKPALPPPLMLLLGLPLSPGALPRPAQADVDLDFPQEPHLVSPSLST 60
DB 1 MLRSKPALPPPLMLLLGLPLSPGALPRPAQADVDLDFPQEPHLVSPSLST 60
QY 61 IDANLATDPRFILLGSPKLTARGLSPAYLRFQGTKTDFLPDKKESTFEERSYQS 120
DB 61 IDANLATDPRFILLGSPKLTARGLSPAYLRFQGTKTDFLPDKKESTFEERSYQS 120
QY 121 QVNODICKGSIIPVVEEKLRLMEPYOQLLRHYOKKFKNSTYSRSVDVLYTFANCS 180
DB 121 QVNODICKGSIIPVVEEKLRLMEPYOQLLRHYOKKFKNSTYSRSVDVLYTFANCS 180
QY 181 GDLIFGALNALTADLQWNSNAQLLDYCSSKGYNI SWEIGNEPNSFLKKADIFINGS 240
DB 181 GDLIFGALNALTADLQWNSNAQLLDYCSSKGYNI SWEIGNEPNSFLKKADIFINGS 240
QY 241 QUGEDYIQLHKLRLKSTFKNATLYGPDVGOPRRKTAAMLKSFLLKAGGEVIDSVTWHYYL 300
DB 241 QUGEDYIQLHKLRLKSTFKNATLYGPDVGOPRRKTAAMLKSFLLKAGGEVIDSVTWHYYL 300
QY 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTRGKKVWLGESSAYGGAPLLSDTFA 360
DB 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTRGKKVWLGESSAYGGAPLLSDTFA 360
QY 361 AGFWMLDLKGLSARNGIEVWNRQVFGAGNYHVDENPDLPDYWLSLFFKLAVGTVM 420
DB 361 AGFWMLDLKGLSARNGIEVWNRQVFGAGNYHVDENPDLPDYWLSLFFKLAVGTVM 420
QY 421 ASVQSKRKRKLRYVHCTNTNPNRKEGDLTYAINLHNTKYRLRPPFSNKQVDXYLL 480
DB 421 ASVQSKRKRKLRYVHCTNTNPNRKEGDLTYAINLHNTKYRLRPPFSNKQVDXYLL 480
QY 481 RPLGPHGLSKSVOLNGITLTKAVDQTLPLMEKPLRGSSILGPARSYSPFVIRNAKVA 540
DB 481 RPLGPHGLSKSVOLNGITLTKAVDQTLPLMEKPLRGSSILGPARSYSPFVIRNAKVA 540
QY 541 ACI 543
DB 541 ACI 543

```

RESULT 2
 AAY57590
 ID AAY57590 standard; protein; 543 AA.

AAV57590;
 02-MAR-2000 (first entry)

DE Human heparanase.
 XX
 KM Human, heparanase; hpa; genetic modification; expression; anticancer;
 KM angiogenesis; anti-angiogenic; antiproliferative; antiviral; antitumor;
 KM anti-atherosclerotic; anti-inflammatory; antineurodegeneration;
 KM heparan sulphate; heparin-binding factor; tumour angiogenesis;
 KM metastasis; wound healing; restenosis; atherosclerosis; inflammation;
 KM neurodegeneration; viral infection; cystic fibrosis; cancer; diagnosis;
 KM micrometastasis; autoimmune lesion; kidney failure.
 XX

OS Homo sapiens.
 XX
 XX WO957244-A1.
 XX
 XX 11-NOV-1999.
 PD
 XX
 XX 29-APR-1999; 99WO-US009256.
 PF
 XX
 PR 01-MAY-1998; 98US-00071618.
 PR 02-MAR-1999; 99US-00260038.
 XX
 XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 PA (FRIE/) FRIEDMAN M M.
 XX
 FI Ben-Artzi H, Ayal-Herskovitz M, Yacoby-Zeevi O, Pecker I;
 FI Peleg Y, Shlom'i Y;
 XX
 DR MPI; 2000-062144/05.
 DR N-PSDB; AAZ39195.
 XX
 PT Engineered cells that express recombinant heparanase, useful
 PT therapeutically, e.g. for treating angiogenesis and to screen for
 PT specific inhibitors, potential anticancer agents.
 PS
 PS Claim 3; Page 107-109; 118pp; English.
 CC
 CC The present invention describes genetically modified cells (A) containing
 CC a polynucleotide (I) that encodes a polypeptide with heparanase activity,
 CC and express recombinant heparanase (II). Heparanase cleaves heparan
 CC sulphate (HS) at specific intrachain sites, resulting in release of
 CC heparin-binding growth factors, enzymes and proteins that are sequestered
 CC by HS in basement membranes, extracellular matrix or cell surfaces. It
 CC may also be implicated in tumour angiogenesis and metastases. (II) is
 CC potentially useful in wound healing and for treating angiogenesis,
 CC restenosis, atherosclerosis, inflammation, neurodegeneration, viral
 CC infection and cystic fibrosis. It can also be used to neutralise heparin
 CC (an alternative to protamine) and to screen for specific inhibitors
 CC (potentially useful for treating cancer and metastases). Antibodies
 CC raised against (II) are used for immunodetection and diagnosis of
 CC micrometastases, autoimmune lesions and kidney failure. (A) provide (II)
 CC in large quantities, in a form that is homogeneously processed and
 CC activated/neutralised by a dedicated protease. The present sequence
 CC represents human heparanase
 XX
 SQ Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 3; Length 543;
 Best Local Similarity 100.0%; Pred. No. 2.5e-273;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MLRSKPALPPPLMLLLGLPLSPGALPRPAQADVDLDFPQEPHLVSPSLST 60
DB 1 MLRSKPALPPPLMLLLGLPLSPGALPRPAQADVDLDFPQEPHLVSPSLST 60
QY 61 IDANLATDPRFILLGSPKLTARGLSPAYLRFQGTKTDFLPDKKESTFEERSYQS 120
DB 61 IDANLATDPRFILLGSPKLTARGLSPAYLRFQGTKTDFLPDKKESTFEERSYQS 120
QY 121 QVNODICKGSIIPVVEEKLRLMEPYOQLLRHYOKKFKNSTYSRSVDVLYTFANCS 180
DB 121 QVNODICKGSIIPVVEEKLRLMEPYOQLLRHYOKKFKNSTYSRSVDVLYTFANCS 180
QY 181 GDLIFGALNALTADLQWNSNAQLLDYCSSKGYNI SWEIGNEPNSFLKKADIFINGS 240
DB 181 GDLIFGALNALTADLQWNSNAQLLDYCSSKGYNI SWEIGNEPNSFLKKADIFINGS 240
QY 241 QUGEDYIQLHKLRLKSTFKNATLYGPDVGOPRRKTAAMLKSFLLKAGGEVIDSVTWHYYL 300
DB 241 QUGEDYIQLHKLRLKSTFKNATLYGPDVGOPRRKTAAMLKSFLLKAGGEVIDSVTWHYYL 300
QY 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTRGKKVWLGESSAYGGAPLLSDTFA 360
DB 301 NGRTATREDPLNPVDLDFISSVQKVFQVVESTRGKKVWLGESSAYGGAPLLSDTFA 360

```

QY 361 AGFWMLDLGLGSARWGIENVKROVFPAGNHYLVDPDPLPDYWLSTLFFKLVGTXYLM 420
 DB 361 AGFWMLDLGLGSARWGIENVKROVFPAGNHYLVDPDPLPDYWLSTLFFKLVGTXYLM 420
 QY 421 ASVQGSKRKRKLRYVYLHCTNTDNPXYKEGDLTLVAIINLHNVTKYLRLPYFSGNKQVDKXYL 480
 DB 421 ASVQGSKRKRKLRYVYLHCTNTDNPXYKEGDLTLVAIINLHNVTKYLRLPYFSGNKQVDKXYL 480
 QY 481 RPLGPHGLLSKSVQVNLGLTKMVDQTLPLMEKRLRGSSIGLPAESYSFFVIRNAKVA 540
 DB 481 RPLGPHGLLSKSVQVNLGLTKMVDQTLPLMEKRLRGSSIGLPAESYSFFVIRNAKVA 540
 QY 541 ACI 543
 DB 541 ACI 543

RESULT 3
 AAB08849
 ID AAB08849 standard; protein; 543 AA.
 AC AAB08849;
 DT 15-JAN-2001 (first entry)
 DE Amino acid sequence of a human heparanase polypeptide.
 KW Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
 KW heparin-binding growth factor; cytokine; neurodegenerative plaque;
 KW wound healing; infection; burn; angiogenesis; restenosis;
 KW atherosclerosis; inflammation; neurodegenerative disease;
 KW Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease.
 OS Homo sapiens.
 PN MO20052178-A1.
 PD 08-SEP-2000.
 XX 14-FEB-2000; 2000WO-US003542.
 PR 01-MAR-1999; 99US-00258892.
 PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 PA (HADA-) HADAST MEDICAL RES SERVICES & DEV.
 PA (FRIE/) FRIEDMAN M M.
 PI Pecker I, Vlodevsky I, Feinstein E;
 WP1; 2000-579289/54.
 N-PSDB; AAA75051.

New polynucleotides encoding a polypeptide having heparanase activity,
 useful in wound healing and in gene therapy, particularly in treating
 tumor, inflammation, autoimmunity, neurodegenerative diseases.
 Claim 22; Fig 1; 152pp; English.

The present sequence represents a human protein with heparanase catalytic
 activity. The heparanase (hpa) polynucleotide is useful in gene therapy,
 particularly in treating tumour, inflammation or autoimmunity.
 Particularly, the polynucleotide is useful in modulating the
 bioavailability of heparin-binding growth factors, cellular responses to
 heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
 interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
 susceptibility to certain viral and some bacterial and protozoa
 infections, or disintegration of neurodegenerative plaques. The
 polynucleotide is also useful in wound healing (e.g. thermal, chemical or
 radiation burns), and in the treatment of angiogenesis, restenosis,
 atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
 Straussler Syndrome or Creutzfeldt-Jakob disease), and some viral,
 bacterial or protozoa infections

XX SQ Sequence 543 AA;
 Query Match 100.0%; Score 2842; DB 3; Length 543;
 Best Local Similarity 100.0%; Pident. No. 2,5e-473;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKRALPPPLMLLLGLGPIPSGALPPPAQOVVDLDFTOEPLHLVSPFLSVT 60
 DB 1 MLRSKRALPPPLMLLLGLGPIPSGALPPPAQOVVDLDFTOEPLHLVSPFLSVT 60
 QY 61 IDANLATDPRFLILGSPKRTTLARGLSPAYLRFSGTKTDFLIDPKKESTFEERSYQOS 120
 DB 61 IDANLATDPRFLILGSPKRTTLARGLSPAYLRFSGTKTDFLIDPKKESTFEERSYQOS 120
 QY 121 QVNODICKYGSIPPDVEBKRLLEMPYQOLLRHHYQKKFKNSYSSSSVDVLYTFANCS 180
 DB 121 QVNODICKYGSIPPDVEBKRLLEMPYQOLLRHHYQKKFKNSYSSSSVDVLYTFANCS 180
 QY 181 GLDLIFGLNLLRTADLQWNSNNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
 DB 181 GLDLIFGLNLLRTADLQWNSNNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
 QY 241 QLGEDYIQLHLKLSKSTFKNAKLYGPDVGQPRRRTAKMLSLFKAGEVIDSVTMHHYLL 300
 DB 241 QLGEDYIQLHLKLSKSTFKNAKLYGPDVGQPRRRTAKMLSLFKAGEVIDSVTMHHYLL 300
 QY 301 NGRITATBEDFLNPVDLIFISSVQKRVQVVESTPGKKWLGERTSSAYGGAPILSDTFA 360
 DB 301 NGRITATBEDFLNPVDLIFISSVQKRVQVVESTPGKKWLGERTSSAYGGAPILSDTFA 360
 QY 361 AGFWMLDLGLGSARWGIENVKROVFPAGNHYLVDPDPLPDYWLSTLFFKLVGTXYLM 420
 DB 361 AGFWMLDLGLGSARWGIENVKROVFPAGNHYLVDPDPLPDYWLSTLFFKLVGTXYLM 420
 QY 421 ASVQGSKRKRKLRYVYLHCTNTDNPXYKEGDLTLVAIINLHNVTKYLRLPYFSGNKQVDKXYL 480
 DB 421 ASVQGSKRKRKLRYVYLHCTNTDNPXYKEGDLTLVAIINLHNVTKYLRLPYFSGNKQVDKXYL 480
 QY 481 RPLGPHGLLSKSVQVNLGLTKMVDQTLPLMEKRLRGSSIGLPAESYSFFVIRNAKVA 540
 DB 481 RPLGPHGLLSKSVQVNLGLTKMVDQTLPLMEKRLRGSSIGLPAESYSFFVIRNAKVA 540
 QY 541 ACI 543
 DB 541 ACI 543

RESULT 4
 AAY52990
 ID AAY52990 standard; protein; 543 AA.
 AC AAY52990;
 DT 21-FEB-2000 (first entry)
 DE Human heparanase protein sequence.
 KW Human; heparanase; hpa; diagnosis; therapy; tumour; cytostatic;
 KW antidiabetic; immunomodulatory; anti-inflammatory; nephrotic;
 KW metastasis; adenocarcinoma; squamous cell carcinoma; teratocarcinoma;
 KW mesothelioma; melanoma; lymphoma; leukemia; cancer; sepsis; diabetes;
 KW inflammation; haemorrhagic nephritis; nephrotic syndrome;
 KW autoimmune disease; anticancer; kidney disease.
 OS Homo sapiens.
 PN MO3957153-A1.
 PD 11-NOV-1999.
 PR 29-APR-1999; 99WO-US009255.

PR 01-MAY-1998; 98US-00071739.

XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASI MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.

XX Pecker I, Vlodavsky I, Friedman Y, Perets T;

XX WPI; 2000-052944/04.

DR N-PSDB; AA33290.

PT Heparanase-specific molecular probes useful for diagnosis and treatment,
XX e.g. of tumors, and for targeted drug delivery.

XX Example; Page 81-82; 90pp; English.

XX The present invention describes heparanase-specific molecular probes,
CC useful for methods of detecting heparanase in situ. The probes and anti-
CC heparanase antibodies are used to detect or quantify the expression of
CC heparanase, for diagnosis and monitoring of diseases (especially
CC metastasis), for treatment of heparanase-associated diseases (e.g.
CC tumors), (adeno)carcinoma, squamous cell carcinoma, teratocarcinoma,
CC mesothelioma, melanoma, lymphoma or leukemia, a solid cancer (or its
CC metastases) derived from liver, prostate, bladder, breast, ovary, cervix,
CC colon, skin, intestine, stomach, uterus and pancreas, kidney disease,
CC diabetes and inflammation, haemorrhagic nephritis, nephrotic syndrome,
CC sepsis and inflammatory or autoimmune disease), for targeted drug
CC delivery (e.g. of anticancer agents) and as research reagents. The
CC present sequence represents human heparanase, which is used in the
XX exemplification of the present invention

XX Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 3; Length 543;

Best Local Similarity 100.0%; Pred. No. 2.5e-273; Mismatches 0; Indels 0; Gaps 0;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKPALPPMLLLGPIGLSPGALPRPAQADVVDDFTQEPHLVSPFLSVT 60

DB 1 MLRSKPALPPMLLLGPIGLSPGALPRPAQADVVDDFTQEPHLVSPFLSVT 60

QY 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFSGRTDPLIDPKKESTFEERSYWG 120

DB 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFSGRTDPLIDPKKESTFEERSYWG 120

QY 121 QVNODICKYGSIPDVEEKLRLWPYQOLLRHYOKKFNSTYSRSVDVLYTFANCS 180

DB 121 QVNODICKYGSIPDVEEKLRLWPYQOLLRHYOKKFNSTYSRSVDVLYTFANCS 180

QY 181 GLDLIFGLNALIRTDADLQWNSNNAQLLDYCSSKGYNI SWEIGNEPNSFLKKADIFINGS 240

DB 181 GLDLIFGLNALIRTDADLQWNSNNAQLLDYCSSKGYNI SWEIGNEPNSFLKKADIFINGS 240

QY 241 QLGEDYIQLHLKLRSTFKNAKLYGPDVGOPRRTATMLSPFKAGSEVDSVTWHYYL 300

DB 241 QLGEDYIQLHLKLRSTFKNAKLYGPDVGOPRRTATMLSPFKAGSEVDSVTWHYYL 300

QY 301 NGRTATREDPLNPVDLIFISSVQKVFQVVESTPGKKWLGETSSAYGGAPLSDTFA 360

DB 301 NGRTATREDPLNPVDLIFISSVQKVFQVVESTPGKKWLGETSSAYGGAPLSDTFA 360

QY 361 AGFWMLDKLGLSARMGIEVVMROVFGAGNYHLVDENFDPLPYWLSLFLKKLVGTKVL 420

DB 361 AGFWMLDKLGLSARMGIEVVMROVFGAGNYHLVDENFDPLPYWLSLFLKKLVGTKVL 420

QY 421 ASVQGSRRRLRYVLIHCTNTDNPYKEGDLTYAINLHNTKYLRLEPYPSNQVQVLYL 480

DB 421 ASVQGSRRRLRYVLIHCTNTDNPYKEGDLTYAINLHNTKYLRLEPYPSNQVQVLYL 480

QY 481 RPLGPGGLSKSVQNLTLKAMDQDTLPLMEKPYLPSSGLPAPSYFFVIRNAKYA 540

DB 481 RPLGPGGLSKSVQNLTLKAMDQDTLPLMEKPYLPSSGLPAPSYFFVIRNAKYA 540

QY 541 ACI 543
DB 541 ACI 543

RESULT 5
ID AAY97635
AAY97635 standard; protein; 543 AA.

XX AAY97635;

DT 20-APR-2001 (first entry)

DE Human heparanase protein sequence.

KW Heparanase; hnp1; wound healing; angiogenesis; restenosis; Scarpe;
KW atherosclerosis; inflammation; pulmonary disease; Alzheimer's disease;
KW neurodegenerative disease; Creutzfeldt-Jakob disease; viral infection;
XX gene therapy; human.

OS Homo sapiens.

EN W020100643-A2.

PD 04-JAN-2001.

PF 19-JUN-2000; 2000WO-11000358.

XX 25-JUN-1999; 99US-0140801P.

XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.

PI Pecker I, Michal I, Itzhaki H;

DR WPI; 2001-137930/14.

PT New polynucleotides and polypeptides that are distantly homologous to
PT heparanase, useful in wound healing, as well as in gene therapy protocols
XX for angiogenesis, restenosis, atherosclerosis, or inflammation.

PS Disclosure; Page 64-65; 67pp; English.

XX This sequence represents a heparanase of the invention. The heparanase
CC DNA and protein sequences are useful in wound healing, angiogenesis,
CC restenosis, atherosclerosis, inflammation, pulmonary diseases,
CC neurodegenerative diseases (such as Scarpe, Alzheimer's disease, and
CC Creutzfeldt-Jakob disease) or viral infections. The heparanase coding
XX sequence is particularly useful in gene therapy

XX Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 4; Length 543;

Best Local Similarity 100.0%; Pred. No. 2.5e-273; Mismatches 0; Indels 0; Gaps 0;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKPALPPMLLLGPIGLSPGALPRPAQADVVDDFTQEPHLVSPFLSVT 60

DB 1 MLRSKPALPPMLLLGPIGLSPGALPRPAQADVVDDFTQEPHLVSPFLSVT 60

QY 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFSGRTDPLIDPKKESTFEERSYWG 120

DB 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFSGRTDPLIDPKKESTFEERSYWG 120

QY 121 QVNODICKYGSIPDVEEKLRLWPYQOLLRHYOKKFNSTYSRSVDVLYTFANCS 180

DB 121 QVNODICKYGSIPDVEEKLRLWPYQOLLRHYOKKFNSTYSRSVDVLYTFANCS 180

QY 181 GLDLIFGLNALIRTDADLQWNSNNAQLLDYCSSKGYNI SWEIGNEPNSFLKKADIFINGS 240

DB 181 GLDLIFGLNALIRTDADLQWNSNNAQLLDYCSSKGYNI SWEIGNEPNSFLKKADIFINGS 240

QY 241 QLGEDYIQLHLKLRSTFKNAKLYGPDVGOPRRTATMLSPFKAGSEVDSVTWHYYL 300

DB 241 QLGEDYIQLHLKLRSTFKNAKLYGPDVGOPRRTATMLSPFKAGSEVDSVTWHYYL 300

Db 241 QLGEDYIQLHLKLRSTFKNAKLYGPDVGOPRRKTAKMLKSGEVLDSVTMHHYYL 300
 Qy 301 NGRTATREDPLNPVDLFISSVQKVFQVVESTPRGKKVWLGETSSAYGGAPLLSDTFA 360
 Db 301 NGRTATREDPLNPVDLFISSVQKVFQVVESTPRGKKVWLGETSSAYGGAPLLSDTFA 360
 Qy 361 AGFWMLDKLGISAMGIEVVNRQVFGAGNYHLVDENFDPLPDYWLSTLFFKKLVGTXYLM 420
 Db 361 AGFWMLDKLGISAMGIEVVNRQVFGAGNYHLVDENFDPLPDYWLSTLFFKKLVGTXYLM 420
 Qy 421 ASVQGSRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNTKYRLRPPFSNKQVDKXYL 480
 Db 421 ASVQGSRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNTKYRLRPPFSNKQVDKXYL 480
 Qy 481 RPLGPHGLSKSVQNLGLTLKMWVDQTLPLMEKPLRPGSSLGLPAPFSYSPFVIRNAKVA 540
 Db 481 RPLGPHGLSKSVQNLGLTLKMWVDQTLPLMEKPLRPGSSLGLPAPFSYSPFVIRNAKVA 540
 Qy 541 ACI 543
 Db 541 ACI 543
 RESULT 6
 ABB07813
 ID ABB07813 standard; protein; 543 AA.
 AC ABB07813;
 DT 03-JUL-2002 (first entry)
 XX Human heparanase sequence.
 DE Human heparanase sequence.
 XX Heparanase; catalytic; cytosolic; antiviral; antibacterial; enzyme;
 KM anti-Protozoan; neuroprotective; heparin; human.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..35
 FT Protein /note= "signal peptide"
 FT Protein 36..543
 FT Protein /note= "mature protein"
 XX
 PN US2002034810-A1.
 XX
 PD 21-MAR-2002.
 XX
 PF 16-AUG-2001; 2001US-00930218.
 XX
 PR 20-SEP-2000; 2000US-00666390.
 XX
 PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 PI Goldsmith O, Pecker I, Vlodavsky I, Michal I, Zcharia E;
 DR WPI; 2002-338926/37.
 XX
 DR Nucleic acid encoding avian and reptile heparanase polypeptide is useful
 PT to treat various heparin-related disorders and the signal peptide is
 PT useful in production of membrane-targeted or secreted recombinant
 PT proteins.
 XX
 PS Disclosure; Fig 1a; 39pp; English.
 XX
 CC The invention relates to an isolated avian and reptile nucleic acid,
 CC encoding a polypeptide with heparanase catalytic activity. The signal
 CC peptide of the nucleic acid can be used to express membrane-associated or
 CC secreted proteins in heterologous expression systems. The encoded
 CC polypeptides can be used to prevent tumour angiogenesis, metastasis and
 CC invasion, and to intervene with pathologies associated with impaired
 CC heparin-binding growth factors, cellular responses to heparin-binding
 CC growth factors and cytokines, cell interaction with plasma lipoproteins,

CC cellular susceptibility to viral, protozoa and bacterial infections or
 CC disintegration of neurodegenerative plaques. The present sequence
 CC represents a human heparanase protein sequence used in similarity studies
 XX
 SQ Sequence 543 AA;
 Query Match 100.0%; Score 2842; DB 5; Length 543;
 Best Local Similarity 100.0%; Pred. No. 2,56-273;
 Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MLRSKDALPPPLMLLLGLPLSPGALPPPAQAOVVDLDFPTQEPRLHVSFISVT 60
 Db 1 MLRSKDALPPPLMLLLGLPLSPGALPPPAQAOVVDLDFPTQEPRLHVSFISVT 60
 Qy 61 IDANLADPPEPLILGSPKRLTLAGSPAYLRGSGTKTPELRDPKKESTFEERSYQOS 120
 Db 61 IDANLADPPEPLILGSPKRLTLAGSPAYLRGSGTKTPELRDPKKESTFEERSYQOS 120
 Qy 121 QVNODICKYGSIPPDVEKRLLEWPYOEOLLRHYOKKFNSTYSRSYDVLTYFANCS 180
 Db 121 QVNODICKYGSIPPDVEKRLLEWPYOEOLLRHYOKKFNSTYSRSYDVLTYFANCS 180
 Qy 181 GLDLIFGLNALRTADLQMNSSNAQLLDYCSSKGYNI SWELGNEPNSFLKKADIPTNGS 240
 Db 181 GLDLIFGLNALRTADLQMNSSNAQLLDYCSSKGYNI SWELGNEPNSFLKKADIPTNGS 240
 Qy 241 QLGSDYIQLHLKLRSTFKNAKLYGPDVGOPRRKTAKMLKSGEVLDSVTMHHYYL 300
 Db 241 QLGSDYIQLHLKLRSTFKNAKLYGPDVGOPRRKTAKMLKSGEVLDSVTMHHYYL 300
 Qy 301 NGRTATREDPLNPVDLFISSVQKVFQVVESTPRGKKVWLGETSSAYGGAPLLSDTFA 360
 Db 301 NGRTATREDPLNPVDLFISSVQKVFQVVESTPRGKKVWLGETSSAYGGAPLLSDTFA 360
 Qy 361 AGFWMLDKLGISAMGIEVVNRQVFGAGNYHLVDENFDPLPDYWLSTLFFKKLVGTXYLM 420
 Db 361 AGFWMLDKLGISAMGIEVVNRQVFGAGNYHLVDENFDPLPDYWLSTLFFKKLVGTXYLM 420
 Qy 421 ASVQGSRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNTKYRLRPPFSNKQVDKXYL 480
 Db 421 ASVQGSRRKRLRVYLHCTNTDNPYKEGDLTLVAINLHNTKYRLRPPFSNKQVDKXYL 480
 Qy 481 RPLGPHGLSKSVQNLGLTLKMWVDQTLPLMEKPLRPGSSLGLPAPFSYSPFVIRNAKVA 540
 Db 481 RPLGPHGLSKSVQNLGLTLKMWVDQTLPLMEKPLRPGSSLGLPAPFSYSPFVIRNAKVA 540
 Qy 541 ACI 543
 Db 541 ACI 543
 RESULT 7
 ADG88800
 ID ADG88800 standard; protein; 543 AA.
 AC ADG88800;
 DT 11-MAR-2004 (first entry)
 XX
 DE Human hpa protein.
 XX
 KW Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
 KW necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2003161823-A1.
 XX
 PD 28-AUG-2003.
 XX
 PF 14-JAN-2003; 2003US-00341582.
 XX
 PR 31-AUG-1998; 98WO-US017954.

PR 01-MAR-1999; 99US-00258892.
PR 06-FEB-2001; 2001US-00776874.
PR 05-SEP-2001; 2001WO-00700830.
PR 19-NOV-2001; 2001US-00988113.

PA (ILAN/) ILAN N.
PA (VLAD/) VLADAVSKY I.
PA (YACO/) YACOBY-ZEEVI O.
PA (PECKE/) PECKER I.
PA (FEIN/) FEINSTEIN E.

PI Ian N, Vlodaevsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;

DR MPI: 2003-897910/82.

DR N-FSDB; ADG88799, ADG88801, ADG88832.

PT Composition for treating a wound comprising recombinant heparanase is
PT useful to induce or accelerate wound healing and induce or accelerate
XX angiogenesis.

PS Claim 2; SEQ ID NO 10; 143bp; English.

CC The present invention relates to methods and compositions for inducing
CC and/or accelerating wound healing via the catalytic activity of
CC heparanase. The invention is used to induce or accelerate a healing
CC process, particularly of an ulcer, burn, laceration, surgical incision,
CC necrosis, pressure wound, diabetic ulcer and to induce or accelerate
CC angiogenesis. The present sequence is human hpa protein.

XX Sequence 543 AA;

Query Match

Best Local Similarity 100.0%; Score 2842; DB 7; Length 543;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDVDFEFQBPPLHVSFSLSVT 60
DB 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVDVDFEFQBPPLHVSFSLSVT 60
QY 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFGCTKTDFLIPDKESFEEBSYWQS 120
DB 61 IDANLATDPRFLILGSPKLTARGLSPAYLRFGCTKTDFLIPDKESFEEBSYWQS 120
QY 121 QVNODICKGSIIPDVEEKLRLWEPYOEQLLREHYOKKFNSTYSRSVUYTYFANCS 180
DB 121 QVNODICKGSIIPDVEEKLRLWEPYOEQLLREHYOKKFNSTYSRSVUYTYFANCS 180
QY 181 GDDLIFGALNALRTADLQWNSNMAQLLDYCSKGYNISWELGNEPNSFLKADIFNGS 240
DB 181 GDDLIFGALNALRTADLQWNSNMAQLLDYCSKGYNISWELGNEPNSFLKADIFNGS 240
QY 241 QLGEDYIOLHLKLRSTFKNAKLYGPDVGQPRRTAKMLKSLKAGGEVIDSTWHHYL 300
DB 241 QLGEDYIOLHLKLRSTFKNAKLYGPDVGQPRRTAKMLKSLKAGGEVIDSTWHHYL 300
QY 301 NGRTATREDPFLNPUTDIFISSVOKVQVVESTTPGKKWLGETSSAYGGADLSDTRA 360
DB 301 NGRTATREDPFLNPUTDIFISSVOKVQVVESTTPGKKWLGETSSAYGGADLSDTRA 360
QY 361 AGFWMLDGLSABMGIEVWVRQVFGAGNYHLVDNEFDLPYWMSLFLPKLVGKTVLM 420
DB 361 AGFWMLDGLSABMGIEVWVRQVFGAGNYHLVDNEFDLPYWMSLFLPKLVGKTVLM 420
QY 421 ASVGGSRKRLKRVYLACTNTDNPRYXEGDLTYAIVMLHNTKYLRLPYPSNKQVDKYL 480
DB 421 ASVGGSRKRLKRVYLACTNTDNPRYXEGDLTYAIVMLHNTKYLRLPYPSNKQVDKYL 480
QY 481 RPLGPHGLSKSVQVNLGLTLKMTDDOTLPLMKELRPSGSLGPAFYSFVFINAKYA 540
DB 481 RPLGPHGLSKSVQVNLGLTLKMTDDOTLPLMKELRPSGSLGPAFYSFVFINAKYA 540
QY 541 ACT 543
DB 541 ACT 543

DB 541 ACT 543

RESULT 8

ID ADL16379 standard; protein; 543 AA.

AC ADL16379;

DT 06-MAY-2004 (first entry)

DE Human heparanase partial protein.

KW Human; heparanase; heparanase-dependent cancer; cancer;
KW autoimmune reaction; inflammation; chromosome 4; enzyme.

OS Homo sapiens.

PN US2003236215-A1.

PD 25-DEC-2003.

PF 09-JUN-2003; 2003US-00456573.

PR 31-AUG-1998; 98MO-US017954.

PR 01-MAR-1999; 99US-00258892.

PR 08-NOV-1999; 99US-00435739.

PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.

PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

DR MPI; 2004-070610/07.

PT New antisense oligonucleotide hybridizable with a polynucleotide encoding
PT a polypeptide with heparanase activity, useful for treating diseases such
PT as cancer and autoimmune disorders.

PS Claim 3; SEQ ID NO 10; 108bp; English.

CC The invention relates to an antisense oligonucleotide (ASO) comprising a
CC polynucleotide or a polynucleotide analogue of at least 10 bases being
CC hybridizable in vivo, under physiological conditions, with a portion of
CC a polynucleotide strand encoding a polypeptide having heparanase
CC catalytic activity. Also included are a method of in vivo downregulating
CC heparanase activity (comprising administering the ASO in vivo), a method
CC (characterized by heparanase activity, comprising administering ASO to
CC the subject), a pharmaceutical composition comprising the ASO and a
CC carrier, an antisense nucleic acid construct (comprising a promoter
CC sequence and a polynucleotide sequence directing the synthesis of an
CC antisense RNA sequence of at least 10 bases being hybridizable in vivo,
CC under physiological conditions, with a polynucleotide strand encoding a
CC polypeptide having heparanase catalytic activity), a method of in vivo
CC downregulating heparanase activity (comprising administering in vivo the
CC antisense nucleic acid construct), a pharmaceutical composition
CC comprising the antisense nucleic acid construct and a carrier, and an
CC analogue of at least 10 bases being hybridizable in vivo, under
CC physiological conditions, with a portion of a polynucleotide strand being
CC characterized by forming at least a portion of an untranslated region
CC (UTR) for a polynucleotide strand encoding a polypeptide having
CC heparanase catalytic activity. The methods and compositions of the
CC present invention are useful for the prevention and/or treatment of
CC diseases or conditions associated with aberrant heparanase activity, such
CC as heparanase-dependent cancer, cancer, autoimmune reaction and
CC inflammation. The gene for human heparanase is located on chromosome 4.
CC The present sequence is a human heparanase protein.

XX Sequence 543 AA;

Query Match

100.0%; Score 2842; DB 8; Length 543;

Best Local Similarity 100.0%; Pred. No. 2,5e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	MLRSXPALPPRLMLLLGRLGRLPSGALPRAPAKOVVDLDFTQERLHVSSFLSYT	60
Db	1 MLRRSPALPPRLMLLLGRLGRLPSGALPRAPAKOVVDLDFTQERLHVSSFLSYT	60
Qy	61 IDANLATDPRFLILGSPKLRTLARGLSPAYRFGCTYTDLFIDPKKESSTFEERSWQS	120
Db	61 IDANLATDPRFLILGSPKLRTLARGLSPAYRFGCTYTDLFIDPKKESSTFEERSWQS	120
Qy	121 QVNODICTGSIIPDVEEKLRLBWPYEOQLLREHYOKKFNKSTYSNBSVDVITYFANCS	180
Db	121 QVNODICTGSIIPDVEEKLRLBWPYEOQLLREHYOKKFNKSTYSNBSVDVITYFANCS	180
Qy	181 GDLIRIGLVNALLRTALQWNSNNAOLLDDYCSKGYNI SWELGNEPNSFLKKADIPTNGS	240
Db	181 GDLIRIGLVNALLRTALQWNSNNAOLLDDYCSKGYNI SWELGNEPNSFLKKADIPTNGS	240
Qy	241 QLGEDVIOLHLKLRKSTFPKNAKLGYBDVQGPFRKAKMLKSFLLAAGEVIDSVYMHYYL	300
Db	241 QLGEDVIOLHLKLRKSTFPKNAKLGYBDVQGPFRKAKMLKSFLLAAGEVIDSVYMHYYL	300
Qy	301 NGRTATREDPLNDVDLIDFISSVQKVPQVVESTREPKKVMLGESTSSAYGGAPLLSDTFA	360
Db	301 NGRTATREDPLNDVDLIDFISSVQKVPQVVESTREPKKVMLGESTSSAYGGAPLLSDTFA	360
Qy	361 AGPMWLDKGLSARPMIEVVMQVFFGAGNHYLVDENBDPLPDVWLSLFFPKVLGTVKVM	420
Db	361 AGPMWLDKGLSARPMIEVVMQVFFGAGNHYLVDENBDPLPDVWLSLFFPKVLGTVKVM	420
Qy	421 ASYVQSGKRRLRVYLHCTYTDNPRXYEGSDLTYYAINTLHNVKYYRLPYFSPNKQVDKYL	480
Db	421 ASYVQSGKRRLRVYLHCTYTDNPRXYEGSDLTYYAINTLHNVKYYRLPYFSPNKQVDKYL	480
Qy	481 RPLGPHGLSKSVQNLGTLTKOVVDQTLPLMEKFLRPGSSGLPAPSYSPFVIRNAKVA	540
Db	481 RPLGPHGLSKSVQNLGTLTKOVVDQTLPLMEKFLRPGSSGLPAPSYSPFVIRNAKVA	540
Qy	541 ACT 543	
Db	541 ACT 543	

RESULT 9
ADM48716
ID ADM48716 standard; protein; 543 AA.

XX	ADM48716;	
AC		
DT	03-JUN-2004	(first entry)
XX		
DE	Human hpa protein #1.	
XX		
KM	Transgenic animal; heparanase; cancer; viral infection; restenosis;	
KM	neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;	
XX	human.	
OS	Homo sapiens.	
XX		
PN	US2003217375-A1.	
XX		
PD	20-NOV-2003.	
XX		
PF	24-FEB-2003; 2003US-00371218.	
XX		
RR	31-AUG-1998; 98WC-US017954.	
PR	01-MAR-1999; 99US-00256892.	
PR	06-FEB-2001; 2001US-00776874.	
PR	19-NOV-2001; 2001US-00986113.	
XX		
PA	(ZCHA.) ZCHARIA E.	
PA	(VLOD.) VLODAVSKY I.	

PA	(METZ/)	METZGER S.	
PA	(PECK/)	PECKER I.	
PA	(ILAN/)	ILAN N.	
PA	(CHAJ/)	CHAJEK-SHAUL T.	
PA	(GOLD/)	GOLDSMIDT O.	
XX			
PI	Zcharia E,	Vlodavsky I,	Metzger S,
PI	Chajek-Shaul T,	Goldschmidt O,	Pecker I,
			Ilán N

DR WPI; 2004-021918/02.
DR N-PSDB; ADM48715, ADM48717.

PT New transgenic non-human animal expressing heparinase, useful as models for human disease, such as cancers, viral infection, neurodegenerative diseases, restenosis, atherosclerosis and pulmonary disorders.

PS Example 1; SEQ ID NO 10; 106pp; English.

The present invention relates to a transgenic non-human animal whose genome comprises an exogenous polynucleotide sequence, including a promoter active in tissues of the non-human, a region encoding a human heparanase, where the promoter and the region encoding human heparanase are operably linked in the exogenous polynucleotide such that human heparanase is expressed in at least a portion of the cells of the non-human animal. The methods and compositions of the present invention are useful for the production of transgenic animals expressing heparanase, to be used as models for human diseases such as cancers, viral infection, reneosols, neurodegenerative diseases, atherosclerosis and pulmonary disorders. The present sequence is human hpa protein used in the exemplification of the invention.

SQ Sequence 543 AA;

Query Match 100.0%; Score 2842; DB 8; Length 543;

```

      0; Mismatches    0; Indels    0; Gaps    0;
Matches 543; Conservative    0;

```

QY	1	MLLRKXPLPPMLMLLLGLPLGRLSPGALPRQAQADVDDLFDFPOEPLHLVSPSLSYT	60
Db	1	MLLRKXPLPPMLMLLLGLPLGRLSPGALPRQAQADVDDLFDFPOEPLHLVSPSLSYT	60
QY	61	IDANLATOBRFLILGSPKLTARGLSPAULRFPGTKTDFLIFDEKKESTFEERSYMQS	120
Db	61	IDANLATOBRFLILGSPKLTARGLSPAULRFPGTKTDFLIFDEKKESTFEERSYMQS	120
QY	121	QYNODICKYGSIPRVEEKLRLWEYQOBLRLREHYQKFKKSTYSRSSVDVLYTTANCS	180
Db	121	QYNODICKYGSIPRVEEKLRLWEYQOBLRLREHYQKFKKSTYSRSSVDVLYTTANCS	180
QY	181	GLDLIFEGNALRLRTADLQWNSNADLLDDYCSKSGYNIEMELGNBENBFLAKADIETNGS	240
Db	181	GLDLIFEGNALRLRTADLQWNSNADLLDDYCSKSGYNIEMELGNBENBFLAKADIETNGS	240
QY	241	QLGEDYIOLHKLRLKRSFKTERKAKLYGBDVGOPRRKTKAKMLKSPFLKAGGEVYDSTWMHHYYL	300
Db	241	QLGEDYIOLHKLRLKRSFKTERKAKLYGBDVGOPRRKTKAKMLKSPFLKAGGEVYDSTWMHHYYL	300
QY	301	NGRTATREDPLNPVDVLDIFISSQVQYFQVVESTPCKTKWLGSTSA YCGGAPLLSDTPA	360
Db	301	NGRTATREDPLNPVDVLDIFISSQVQYFQVVESTPCKTKWLGSTSA YCGGAPLLSDTPA	360
QY	361	AGFWMLDXGLSARWGEIYVWQVFPFAGNYHLVDENFDPLPDYWLSTLLFKKLVGTRKVLH	420
Db	361	AGFWMLDXGLSARWGEIYVWQVFPFAGNYHLVDENFDPLPDYWLSTLLFKKLVGTRKVLH	420
QY	421	ASVQSGKRRKRLRYVLAHCTNTDNPARKKEGDLTYALNLHVTKYLRLYPFPFSNKQVQKYYL	480
Db	421	ASVQSGKRRKRLRYVLAHCTNTDNPARKKEGDLTYALNLHVTKYLRLYPFPFSNKQVQKYYL	480
QY	481	RPLGEGHLLSKSVQNLGTLTKXWVDQULPRLMEKPLRPGSSGLPASFYSFVYTRNAKVA	540
Db	481	RPLGEGHLLSKSVQNLGTLTKXWVDQULPRLMEKPLRPGSSGLPASFYSFVYTRNAKVA	540

XX PS Claim 22; Page 122-123; 152pp; English.
XX CC The present sequence represents a human protein with heparanase catalytic
XX CC activity. The heparanase (hpa) polynucleotide is useful in gene therapy,
XX CC particularly in treating tumour, inflammation or autoimmunity.
XX CC Particularly, the polynucleotide is useful in modulating the
XX CC bioavailability of heparin-binding growth factors, cellular responses to
XX CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
XX CC interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
XX CC susceptibility to certain viral and some bacterial and protozoa
XX CC infections, or disintegration of neurodegenerative plaques. The
XX CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
XX CC radiation burns), and in the treatment of angiogenesis, restenosis,
XX CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
XX CC Strausler Syndrome or Creutzfeldt-Jakob disease), and some viral,
XX CC bacterial or protozoa infections
SQ Sequence 592 AA;
Query Match 100.0%; Score 2842; DB 3; Length 592;
Best Local Similarity 100.0%; Pred. No. 2.9e-273; Indels 0; Gaps 0;
Matches 543; Conservative 0; Mismatches 0;
QY 1 MLRSKPALPPMLLLGLGPIGSPGALPPPAQADVDDFTQEPHLHVSFSLSVT 60
DB 50 MLRSKPALPPMLLLGLGPIGSPGALPPPAQADVDDFTQEPHLHVSFSLSVT 109
QY 61 IDANLATDPRLLILGSPKLTTLARGLSPAYLRFGTGTDFLIFDPKKESTFEERSYQOS 120
DB 110 IDANLATDPRFLILGSPKLTTLARGLSPAYLRFGTGTDFLIFDPKKESTFEERSYQOS 169
QY 121 QVNODICKYGSIPPDVEEKLRLFWPYQOLLRHHYQKKFNKSTYSRSSVDVLYTFANCS 180
DB 170 QVNODICKYGSIPPDVEEKLRLFWPYQOLLRHHYQKKFNKSTYSRSSVDVLYTFANCS 229
QY 181 GLDLIFGLNALRLTADLQMNSSNAQLLDYCSSKGYNSWEIGNEPNSFLKKADIFINGS 240
DB 230 GLDLIFGLNALRLTADLQMNSSNAQLLDYCSSKGYNSWEIGNEPNSFLKKADIFINGS 289
QY 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300
DB 290 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 349
QY 301 NGRTATREDPLNPVLDLIFISSVQKVFQVVESTRGKVMWLGFTSSAYGGGAPLLSDTFA 360
DB 350 NGRTATREDPLNPVLDLIFISSVQKVFQVVESTRGKVMWLGFTSSAYGGGAPLLSDTFA 409
QY 361 AGFMWLDKLGASARWGEIEMVNRQVFFGAGNYLVENFDPLPDYMLSLFFKKLVGTXYLM 420
DB 410 AGFMWLDKLGASARWGEIEMVNRQVFFGAGNYLVENFDPLPDYMLSLFFKKLVGTXYLM 469
QY 421 ASVQSSKRRKRLVYLHCTNTDNPRYKEGDLTYAINHNTCYLRLPYPFSSNKQVXYTL 480
DB 470 ASVQSSKRRKRLVYLHCTNTDNPRYKEGDLTYAINHNTCYLRLPYPFSSNKQVXYTL 529
QY 481 RPLGSHGLLSKSVQVNGTLLKXVNDQDTPLPMEKELRFGSSGLPAFSYSPFVIRNAYCA 540
DB 530 RPLGSHGLLSKSVQVNGTLLKXVNDQDTPLPMEKELRFGSSGLPAFSYSPFVIRNAYCA 589
QY 541 ACI 543
DB 590 ACI 592
RESULT 12
ADG88804 ID ADG88804 standard; protein; 592 AA.
XX AC ADG88804;
XX DT 11-MAR-2004 (first entry)
XX

DE Human SK-hep1 protein.
XX Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
XX necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy.
XX Homo sapiens.
XX US2003161823-A1.
XX 28-AUG-2003.
XX 14-JAN-2003; 2003US-00341582.
XX 31-AUG-1998; 98WO-US017954.
XX 01-MAR-1999; 99US-00258892.
XX 06-FEB-2001; 2001US-00776874.
XX 05-SEP-2001; 2001WO-IL000830.
XX 19-NOV-2001; 2001US-00988113.
XX (ILAN/) ILAN N.
XX (VLOD/) VLODAVSKY I.
XX (YACO/) YACOBY-ZEEVI O.
XX (PECK/) PECKER I.
XX (FEIN/) FEINSTEIN E.
PI Ilan N, Vladaveky I, Yacoby-Zeevi O, Pecker I, Feinstein E;
DR WPI; 2003-897910/82.
DR N-PSDB; ADG88803, ADG88805.
PT Composition for treating a wound comprising recombinant heparanase is
PT useful to induce or accelerate wound healing and induce or accelerate
PT angiogenesis.
PS Claim 2; SEQ ID NO 14; 143pp; English.
XX The present invention relates to methods and compositions for inducing
XX and/or accelerating wound healing via the catalytic activity of
XX heparanase. The invention is used to induce or accelerate a healing
XX process, particularly of an ulcer, burn, laceration, surgical incision,
XX necrosis, pressure wound, diabetic ulcer and to induce or accelerate
XX angiogenesis. The present sequence is human SK-hep1 protein.
SQ Sequence 592 AA;
Query Match 100.0%; Score 2842; DB 7; Length 592;
Best Local Similarity 100.0%; Pred. No. 2.9e-273; Indels 0; Gaps 0;
Matches 543; Conservative 0; Mismatches 0;
QY 1 MLRSKPALPPMLLLGLGPIGSPGALPPPAQADVDDFTQEPHLHVSFSLSVT 60
DB 50 MLRSKPALPPMLLLGLGPIGSPGALPPPAQADVDDFTQEPHLHVSFSLSVT 109
QY 61 IDANLATDPRLLILGSPKLTTLARGLSPAYLRFGTGTDFLIFDPKKESTFEERSYQOS 120
DB 110 IDANLATDPRLLILGSPKLTTLARGLSPAYLRFGTGTDFLIFDPKKESTFEERSYQOS 169
QY 121 QVNODICKYGSIPPDVEEKLRLFWPYQOLLRHHYQKKFNKSTYSRSSVDVLYTFANCS 180
DB 170 QVNODICKYGSIPPDVEEKLRLFWPYQOLLRHHYQKKFNKSTYSRSSVDVLYTFANCS 229
QY 181 GLDLIFGLNALRLTADLQMNSSNAQLLDYCSSKGYNSWEIGNEPNSFLKKADIFINGS 240
DB 230 GLDLIFGLNALRLTADLQMNSSNAQLLDYCSSKGYNSWEIGNEPNSFLKKADIFINGS 289
QY 241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 300
DB 290 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGQPRRTAKMLKSFLLKAGGEVIDSVTWHYYL 349
QY 301 NGRTATREDPLNPVLDLIFISSVQKVFQVVESTRGKVMWLGFTSSAYGGGAPLLSDTFA 360
DB 350 NGRTATREDPLNPVLDLIFISSVQKVFQVVESTRGKVMWLGFTSSAYGGGAPLLSDTFA 409

QY 361 AGFMWLDKLGISARMGIEVVRQVFPAGNHYLVNDENPDLDPYWSLTFPKLVGTXYLM 420
DB 410 AGFMWLDKLGISARMGIEVVRQVFPAGNHYLVNDENPDLDPYWSLTFPKLVGTXYLM 469
QY 421 ASVQSKRRKRLRVYIHCNTNDNPRYKEGDLTYA INLNHYTKYLRLPYPSNKOVDXYLM 480
DB 470 ASVQSKRRKRLRVYIHCNTNDNPRYKEGDLTYA INLNHYTKYLRLPYPSNKOVDXYLM 529
QY 481 RPLGPHGLSKSVQNLNGTLTKAVDDQTLPLMEKPLRGSSSLGIPAFYSFFVIRNAKVA 540
DB 530 RPLGPHGLSKSVQNLNGTLTKAVDDQTLPLMEKPLRGSSSLGIPAFYSFFVIRNAKVA 589
QY 541 ACT 543
DB 590 ACT 592

RESULT 13
ADL16383
ID ADL16383 standard; protein, 592 AA.
AC ADL16383;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heparanase full length protein.
XX
KW Human, heparanase; heparanase-dependent cancer; cancer;
KW autoimmune reaction; inflammation; chromosome 4; enzyme.
XX
OS Homo sapiens.
PN US2003236215-A1.
XX
PD 25-DEC-2003.
XX
PF 09-JUN-2003; 2003US-00456573.
XX
PR 31-AUG-1998; 98WO-US017954.
PR 01-MAR-1999; 99US-00258892.
PR 08-NOV-1999; 99US-00435739.
XX
PA (INST-) INSTGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADAST MEDICAL RES SERVICES & DEV.
PI Becker I, Vlodevsky I, Feinstein E;
XX
DR WPI; 2004-070610/07.
XX
PT New antisense oligonucleotide hybridizable with a polynucleotide encoding
PT a polypeptide with heparanase activity, useful for treating diseases such
PT as cancer and autoimmune disorders.
XX
PS Claim 3; SEQ ID NO 14; 108bp; English.
XX
XX

The invention relates to an antisense oligonucleotide (ASO) comprising a polynucleotide or a polynucleotide analogue of at least 10 bases being hybridizable in vivo, under physiological conditions, with a portion of a polynucleotide strand encoding a polypeptide having heparanase catalytic activity. Also included are a method of in vivo downregulating heparanase activity (comprising administering the ASO in vivo), a method (characterised by heparanase activity, comprising administering ASO to the subject), a pharmaceutical composition comprising the ASO and a carrier, an antisense nucleic acid construct (comprising the ASO and a sequence and a polynucleotide sequence directing the synthesis of an antisense RNA sequence of at least 10 bases being hybridizable in vivo, under physiological conditions, with a polynucleotide strand encoding a polypeptide having heparanase catalytic activity), a method of in vivo downregulating heparanase activity (comprising administering in vivo the antisense nucleic acid construct), a pharmaceutical composition comprising the antisense nucleic acid construct and a carrier, and an antisense oligonucleotide comprising a polynucleotide or a polynucleotide

CC analogue of at least 10 bases being hybridizable in vivo, under
CC physiological conditions, with a portion of a polynucleotide strand being
CC characterised by forming at least a portion of an untranslated region
CC (UTR) for a polynucleotide strand encoding a polypeptide having
CC heparanase catalytic activity. The methods and compositions of the
CC present invention are useful for the prevention and/or treatment of
CC diseases or conditions associated with aberrant heparanase activity, such
CC as heparanase-dependent cancer, cancer, autoimmune reaction and
CC inflammation. The gene for human heparanase is located on chromosome 4.
XX The present sequence is a human heparanase protein.

Sequence 592 AA;

Query Match 100.0%; Score 2842; DB 8; Length 592;
Best Local Similarity 100.0%; Pred. No. 2.9e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVVDLPFTQEPHLVSPFLSYT 60
DB 50 MLRSKRALPPPLMLLLGLPLSPGALPRPAQADVVDLPFTQEPHLVSPFLSYT 109
QY 61 IDANLATDPRFLLILGSPKRTARGLSPAYLARFGTKTDFLIPDKKSTFEERSYQS 120
DB 110 IDANLATDPRFLLILGSPKRTARGLSPAYLARFGTKTDFLIPDKKSTFEERSYQS 169
QY 121 QVNODICKYGIIPDVEEKLRLMPYQEOQLLREHYQKKFKNSTYSRSSVDVLYTFANCS 180
DB 170 QVNODICKYGIIPDVEEKLRLMPYQEOQLLREHYQKKFKNSTYSRSSVDVLYTFANCS 229
QY 181 GLDLIFGLNALRLTALQWNSNAQILLDYSSKGYNI SWEIGNPNFLKKADIFINGS 240
DB 230 GLDLIFGLNALRLTALQWNSNAQILLDYSSKGYNI SWEIGNPNFLKKADIFINGS 289
QY 241 QLGEDYIQHLKLRKSTFNKATLYGPDVGQPRKTAKLKSLKAGGEVIDSYMHNYL 300
DB 290 QLGEDYIQHLKLRKSTFNKATLYGPDVGQPRKTAKLKSLKAGGEVIDSYMHNYL 349
QY 301 NGRTAREDFLNPDLDFISSVQVQVFOVESTPRKKVWLGETSSAYGGAPLLSDTFA 360
DB 350 NGRTAREDFLNPDLDFISSVQVQVFOVESTPRKKVWLGETSSAYGGAPLLSDTFA 409
QY 361 AGFMWLDKLGISARMGIEVVRQVFPAGNHYLVNDENPDLDPYWSLTFPKLVGTXYLM 420
DB 410 AGFMWLDKLGISARMGIEVVRQVFPAGNHYLVNDENPDLDPYWSLTFPKLVGTXYLM 469
QY 421 ASVQSKRRKRLRVYIHCNTNDNPRYKEGDLTYA INLNHYTKYLRLPYPSNKOVDXYLM 480
DB 470 ASVQSKRRKRLRVYIHCNTNDNPRYKEGDLTYA INLNHYTKYLRLPYPSNKOVDXYLM 529
QY 481 RPLGPHGLSKSVQNLNGTLTKAVDDQTLPLMEKPLRGSSSLGIPAFYSFFVIRNAKVA 540
DB 530 RPLGPHGLSKSVQNLNGTLTKAVDDQTLPLMEKPLRGSSSLGIPAFYSFFVIRNAKVA 589
QY 541 ACT 543
DB 590 ACT 592

RESULT 14
ADM48720
ID ADM48720 standard; protein, 592 AA.
AC ADM48720;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human SK-hepl hpa protein.
XX
KW Transgenic animal; heparanase; cancer; viral infection; restenosis;
KW neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;
KW human.
XX
OS Homo sapiens.

```

XX  US2003217375-A1.
PN
XX
PD  20-NOV-2003.
XX
PF  24-FEB-2003; 2003US-00371218.
XX
PR  31-AUG-1998; 98WO-US017954.
PR  01-MAR-1999; 99US-00258892.
PR  06-FEB-2001; 2001US-00776874.
PR  19-NOV-2001; 2001US-00988113.
XX
XX  (ZCHARA/) ZCHARIA E.
PA  (VL0D/) VL0DASKY I.
PA  (METZG/) METZGER S.
PA  (PECKE/) PECKER I.
PA  (ILAN/) ILAN N.
PA  (CHAJ/) CHAJER-SHAUL T.
PA  (GOLD/) GOLDSHMIDT O.
XX
PI  Zcharia E, Vlodayevy I, Metzger S, Pecker I, Ilan N;
PI  Chajek-Shaul T, Goldshmidt O;
DR  WI; 2004-021918/02.
DR  N-Psdb; ADM48719, ADM48721.
XX
PT  New transgenic non-human animal expressing heparinase, useful as models
PT  for human disease, such as cancers, viral infection, neurodegenerative
PT  diseases, restenosis, atherosclerosis and pulmonary disorders.
XX
PS  Example 6; SEQ ID NO 14; 106pp; English.
XX
CC  The present invention relates to a transgenic non-human animal whose
CC  genome comprises an exogenous polynucleotide sequence, including a
CC  promoter active in tissues of the non-human, a region encoding a human
CC  heparanase, where the promoter and the region encoding human heparanase
CC  are operably linked in the exogenous polynucleotide such that human
CC  heparanase is expressed in at least a portion of the cells of the non-
CC  human animal. The methods and compositions of the present invention are
CC  useful for the production of transgenic animals expressing heparanase, to
CC  be used as models for human diseases such as cancers, viral infection,
CC  restenosis, neurodegenerative diseases, atherosclerosis and pulmonary
CC  disorders. The present sequence is human SK-hep1 hpa protein used in the
CC  exemplification of the invention.
XX
SQ  Sequence 592 AA;
Query Match 100.0%; Score 2842; DB 8; Length 592;
Best Local Similarity 100.0%; Pred. No. 2,9e-273;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  1 MLNRSKPALPPPLMLLLGPIGPSGALPRPAQADVDVDDFTQEPHLHVSPEFLSVT 60
DB  50 MLNRSKPALPPPLMLLLGPIGPSGALPRPAQADVDVDDFTQEPHLHVSPEFLSVT 109
QY  61 IDANATPBRPLILGSPKRLTARGLSPAYRREGCTDPLIPPKKESTFEESYQOS 120
DB  110 IDANATPBRPLILGSPKRLTARGLSPAYRREGCTDPLIPPKKESTFEESYQOS 169
QY  121 QVNODICRYGSIIPVVEEKLRLLEMPYQEQOLLREHYOKKFKNSTYRSRSVDVLYTFANCS 180
DB  170 QVNODICRYGSIIPVVEEKLRLLEMPYQEQOLLREHYOKKFKNSTYRSRSVDVLYTFANCS 229
QY  181 GLDLIFGNALRLTADLQWNSSNAQLLIDYSSSKQYINISWELGNEPNSFLKKADIFINGS 240
DB  230 GLDLIFGNALRLTADLQWNSSNAQLLIDYSSSKQYINISWELGNEPNSFLKKADIFINGS 289
QY  241 QLGEBYIOLHLKLRSTFKNAKLYGPDVGQPRKTAUKLSLTKGSGVINSVTHNYL 300
DB  290 QLGEBYIOLHLKLRSTFKNAKLYGPDVGQPRKTAUKLSLTKGSGVINSVTHNYL 349
QY  301 NGRTATREDPLNPVDLIFISSVQKVFQVESTPRGKKVWLGETSBAVGGAPLLSDTFA 360

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DB  350 NGRTATREDPLNPVDLIFISSVQKVFQVESTPRGKKVWLGETSBAVGGAPLLSDTFA 409
QY  361 AGFWMLDKLIGLSARMGIEVWVRQVFGAGNVLVDENFDPLPDYMLSLFLPKLVGTXYLM 420
DB  410 AGFWMLDKLIGLSARMGIEVWVRQVFGAGNVLVDENFDPLPDYMLSLFLPKLVGTXYLM 469
QY  421 ASVQSRKRLRVYLHCTNTDNPVYKSGDLTLVAIINLHNTKYRLPLPFSNKQVDXYL 480
DB  470 ASVQSRKRLRVYLHCTNTDNPVYKSGDLTLVAIINLHNTKYRLPLPFSNKQVDXYL 529
QY  481 RPLGPHGLSKSVQNLGTLTMMVDQTLPLMEKPLRPGSSGLPAPSYSPFYTRNAKVA 540
DB  530 RPLGPHGLSKSVQNLGTLTMMVDQTLPLMEKPLRPGSSGLPAPSYSPFYTRNAKVA 589
QY  541 ACI 543
DB  590 ACI 592
RESULT 15
AA17082
ID AA17082 standard; protein; 543 AA.
AC AA17082;
XX
DT  21-JUL-1999 (first entry)
DE
XX  Human heparanase enzyme.
XX  Heparanase; endoglucuronidase; heparan sulfate proteoglycan; enzyme;
XX  metastasis; angiogenesis; wound healing; angioplasty-induced restenosis;
XX  atherosclerosis; atherosclerosis; inflammation; tissue development;
XX  human; HSPG.
XX
XX  Homo sapiens.
XX  WO9921975-A1.
XX  06-MAY-1999.
XX
XX  28-OCT-1998; 98WO-AU000898.
XX
XX  28-OCT-1997; 97AU-00000062.
XX  09-DEC-1997; 97AU-00000812.
XX
XX  (AUSU ) UNIV AUSTRALIAN NAT.
XX
XX  Freeman CG, Hulett MD, Parish CR, Hamdorf BJ;
XX  WI; 1999-312956/26.
XX  N-Psdb; AAX37259.
XX
PT  Polynucleotides encoding mammalian endoglucuronidases, especially
PT  heparanases, useful to promote wound healing.
PS  Claim 6; Page 69-73; 112pp; English.
XX
CC  The invention relates to nucleic acid sequences that encode heparanase
CC  enzymes having endoglucuronidase activity. Recombinant heparanases are
CC  capable of removing the HS side chain from heparan sulfate proteoglycan
CC  (HSPG). Sulfated oligosaccharides, sulphates or HSPG can be used to
CC  inhibit heparanase, this is useful for treatment of a physiological or
CC  medical condition associated with elevated heparanase activity such as
CC  metastasis, angiogenesis, wound healing, angioplasty-induced restenosis,
CC  atherosclerosis, atherosclerosis and inflammation. The human, murine and
CC  rat heparanases can be used to enhance wound healing, especially
CC  associated with tissue development and repair. The conditions mentioned
CC  above can be diagnosed using specific antibodies, and also using primers
CC  and probes specific for the heparanase polynucleotides. Other uses of the
CC  heparanases include sequencing sulfated molecules such as HSPG. The
CC  present sequence represents a human heparanase
SQ  Sequence 543 AA;

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Query Match 99.9%; Score 2838; DB 2; Length 543;
 Best Local Similarity 99.8%; Fred. No. 6.2e-273;
 Matches 542; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MLRSKPALPPMLMLLLGPLSPGALPRPAQADVDLDFFTQEPHLVSPSPLSVT 60
Db      1 MLRSKPALPPMLMLLLGPLSPGALPRPAQADVDLDFFTQEPHLVSPSPLSVT 60
QY      61 IDANLATDPRFLILGSPKRLTLARGLSPAYIRFGTITDPLIPDPKKESTFEERSYMQS 120
Db      61 IDANLATDPRFLILGSPKRLTLARGLSPAYIRFGTITDPLIPDPKKESTFEERSYMQS 120
QY      121 QVNODICKYGSIPPDVEEKLRLMPYOBQLLRHYOKKPKNSYSSSVDTYTPANGS 180
Db      121 QVNODICKYGSIPPDVEEKLRLMPYOBQLLRHYOKKPKNSYSSSVDTYTPANGS 180
QY      181 GLDLIFGINALLRTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
Db      181 GLDLIFGINALLRTADLQWSSNAQLLDYCSSKGYNISWELGNEPNSFLKKADIFINGS 240
QY      241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGOPRRKTAKMLKSLKAGGEVIDSVTHHYYL 300
Db      241 QLGEDYIQLHKLRLKSTFKNAKLYGPDVGOPRRKTAKMLKSLKAGGEVIDSVTHHYYL 300
QY      301 NGRTATREDPLNPVDLIFISSVQKVFQVVESTRPGKRWLGRTSSAYGGAPLISDTPA 360
Db      301 NGRTATREDPLNPVDLIFISSVQKVFQVVESTRPGKRWLGRTSSAYGGAPLISDTPA 360
QY      361 AGFWMLDKLGLSARMGIEVVMROVFGAGNYHLVDENFDPLPDYWSLFLFKLVGTXYLM 420
Db      361 AGFWMLDKLGLSARMGIEVVMROVFGAGNYHLVDENFDPLPDYWSLFLFKLVGTXYLM 420
QY      421 ASVOGSKRRRLRYLHCTNTDNPYKSGDLTYAINLHNVTKYLRLEYPFSNKQVDKYL 480
Db      421 ASVOGSKRRRLRYLHCTNTDNPYKSGDLTYAINLHNVTKYLRLEYPFSNKQVDKYL 480
QY      481 RPLGPHGLLSKSYQNLGTLTKWVDQTLPLMEKPLRPSSSLGLPAFSYSPFVIRNAKVA 540
Db      481 RPLGPHGLLSKSYQNLGTLTKWVDQTLPLMEKPLRPSSSLGLPAFSYSPFVIRNAKVA 540
QY      541 ACT 543
Db      541 ACT 543

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Search completed: February 28, 2005, 05:56:40
 Job time : 176 secs

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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 23:09:46 ; Search time 7263 Seconds
(without alignment)
11481.678 Million cell updates/sec

Title: US-10-786-149-1
Perfect score: 1721
Sequence: 1 ctgagcttcgactctccg.....atactagctcgcacacg 1721

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_dr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1721	100.0	1721 6	AR080679 Sequence
2	1721	100.0	1721 6	AR080680 Sequence
3	1721	100.0	1721 6	AR125603 Sequence
4	1721	100.0	1721 6	AR125604 Sequence
5	1721	100.0	1721 6	BD193236 Heparanas
6	1721	100.0	1721 6	BD193237 Heparanas
7	1721	100.0	1721 6	BD205238 Cells gen
8	1721	100.0	1721 6	BD205239 Cells gen
9	1721	100.0	1721 6	AR194189 Sequence
10	1721	100.0	1721 6	AR194190 Sequence
11	1721	100.0	1721 6	AR221285 Sequence
12	1721	100.0	1721 6	AR221286 Sequence
13	1721	100.0	1721 6	AR243203 Sequence
14	1721	100.0	1721 6	AR243204 Sequence
15	1721	100.0	1721 6	AR287435 Sequence
16	1721	100.0	1721 6	AR287436 Sequence
17	1721	100.0	1721 6	AR438812 Sequence
18	1721	100.0	1721 6	AR438813 Sequence
19	1721	100.0	1721 6	AR478814 Sequence

20	1721	100.0	1721 6	AR478815 Sequence
21	1721	100.0	1721 6	BD074427 Polynucle
22	1721	100.0	1721 6	BD074428 Polynucle
23	1719.4	99.9	1721 6	CO840766 Sequence
24	1719.4	99.9	1721 6	CO840768 Sequence
25	1719.4	99.9	1721 6	CO840858 Sequence
26	1719.4	99.9	1721 6	CO840860 Sequence
27	1719.4	99.9	1721 6	AR438815 Sequence
28	1719.4	99.9	1721 6	AR438816 Sequence
29	1719.4	99.9	1721 6	BD074430 Polynucle
30	1719.4	99.9	1721 6	BD074431 Polynucle
31	1717.8	99.8	1758 9	AF144325 Homo sapi
32	1717.8	99.8	1758 9	CO840770 Sequence
33	1717.8	99.8	1758 9	CO840772 Sequence
34	1717.8	99.8	1758 9	CO840862 Sequence
35	1717.8	99.8	1758 9	CO840864 Sequence
36	1713	99.5	1722 6	AX136167 Sequence
37	1713	99.5	1722 6	BD123536 Secretory
38	1713	99.5	1722 9	AK075400 Homo sapi
39	1694.6	98.5	1713 6	AR156691 Sequence
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41	1694.6	98.5	1713 6	AX034643 Sequence
42	1688.8	98.1	1723 6	AR156692 Sequence
43	1688.8	98.1	1723 6	BD226825 Isolated
44	1688.8	98.1	1723 6	AX034645 Sequence
45	1686.8	98.0	3726 6	AR235866 Sequence

ALIGNMENTS

RESULT 1	LOCUS	SEQUENCE	9	FROM PATENT US 5968822.	DNA	LINEAR	PAT 31-AUG-2000
AR080679	Sequence	9	from patent US 5968822.				
AR080679	Sequence	9	from patent US 5968822.				
AR080679.1	GI.10007409						
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 1721)						
AUTHORS	Pecker, I., Vlodavsky, I. and Feinstein, E.						
TITLE	Polynucleotide encoding a polypeptide having heparanase activity and expression of same in transduced cells						
JOURNAL	Patent: US 5968822-A, 9 19-Oct-1999;						
FEATURES	Location/Qualifiers						
source	1..1721						
ORIGIN	/organism="unknown"						
	/mol_type="unassigned DNA"						

Query Match	100.0%	Score 1721;	DB 6;	Length 1721;
Best Local Similarity	100.0%	Pred. No. 0;		
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QY	1	CTGAGCTTCGACTCTCCGCTGCGGCGAGCTGCGGGGAGCAAGTGAAGCCA	60	
DB	1	CTGAGCTTCGACTCTCCGCTGCGGCGAGCTGCGGGGAGCAAGTGAAGCCA	60	
QY	61	AGATGCTGCTGCTCGAAGCTGCGGCTGCGGCGGCTGATGCTGCTGCGGCG	120	
DB	61	AGATGCTGCTGCTCGAAGCTGCGGCTGCGGCGGCTGATGCTGCTGCGGCG	120	
QY	121	CGCTGGTCCCTCTCTCCCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG	180	
DB	121	CGCTGGTCCCTCTCTCCCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG	180	
QY	181	ACCTGCACTTCCTCAACCAAGAGCGGCTGCAACCTGAGAGCCCTGCTGCTCA	240	
DB	181	ACCTGCACTTCCTCAACCAAGAGCGGCTGCAACCTGAGAGCCCTGCTGCTCA	240	
QY	241	CAATTGACGCAACTGCGCAGCAGCCGCGTTCCTCATCTCTGCTGCTCAAGC	300	

Db	241	CCATGAGCCCACTGGCCAGGACCCGGCTTCTCATCTCTCTGAGTTCTCAAAAGC	300
Qy	301	TTGGAACCTGGCCAGAGGCTTGTCTCTGCTGATCTGAGGTTGGTGCCACCAAGACAG	360
Db	301	TTGGAACCTGGCCAGAGGCTTGTCTCTGCTGATCTGAGGTTGGTGCCACCAAGACAG	360
Qy	361	ACTTCTTAATTTTGCATCCCAAGAGATCAACCTTGAAGAGAGAGTTACTGGCAAT	420
Db	361	ACTTCTTAATTTTGCATCCCAAGAGATCAACCTTGAAGAGAGAGTTACTGGCAAT	420
Qy	421	CTGAAGTCAACCAAGATTTTGCATATATGATTCATCCCTCTGATGTGAGAGAGAT	480
Db	421	CTGAAGTCAACCAAGATTTTGCATATATGATTCATCCCTCTGATGTGAGAGAGAT	480
Qy	481	TACGTTGGAATGAGGCTTACCAAGAGATTTGATCTCCGAGAACCTACCAAAAAGT	540
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Qy	541	TCAAGAACAGACCTTACTCAAGAGCTGTGATGATGCTATACATTTTGCAAACTGCT	600
Db	541	TCAAGAACAGACCTTACTCAAGAGCTGTGATGATGCTATACATTTTGCAAACTGCT	600
Qy	601	CAGAGCTGACCTGATCTTGGCTTAATGCGTTATTAAGAACAGCAATTTGCAAGTGA	660
Db	601	CAGAGCTGACCTGATCTTGGCTTAATGCGTTATTAAGAACAGCAATTTGCAAGTGA	660
Qy	661	ACAGTTCTAATGCTAGTTGCTCTGAGTACTGCTCTTCCAAAGGGATTAACATTTCTT	720
Db	661	ACAGTTCTAATGCTAGTTGCTCTGAGTACTGCTCTTCCAAAGGGATTAACATTTCTT	720
Qy	721	GGAACTAGGCAATGAACTTACATTTCTTAAAGAGGCTGATTTTTCATCAATGAGT	780
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Qy	841	ATGCAAACTCTATGCTCTGATGTTGCTCAGCTTCGAAGAAAGCGCTTAAGATGCTGA	900
Db	841	ATGCAAACTCTATGCTCTGATGTTGCTCAGCTTCGAAGAAAGCGCTTAAGATGCTGA	900
Qy	901	AGAGCTTCTGAAGGCTGTGAGAGAGATTAAGTGAATGATCACTCACTACTATTT	960
Db	901	AGAGCTTCTGAAGGCTGTGAGAGAGATTAAGTGAATGATCACTCACTACTATTT	960
Qy	961	TGAATGAGCGGACTGCTACAGGAGATTTTCTAAACCTCTGATGATTTGAATTTTAA	1020
Db	961	TGAATGAGCGGACTGCTACAGGAGATTTTCTAAACCTCTGATGATTTTGAATTTTAA	1020
Qy	1021	TTTCATCTGTGCAAAAAGTTTCCAGGTGTTGAGAGACACAGGCTTGGCAAGAGTCT	1080
Db	1021	TTTCATCTGTGCAAAAAGTTTCCAGGTGTTGAGAGACACAGGCTTGGCAAGAGTCT	1080
Qy	1081	GGTTAGAGAAACAAGCTCTGCAATATGAGAGCGGAGCGCTTGTCTATCCGACCTTTG	1140
Db	1081	GGTTAGAGAAACAAGCTCTGCAATATGAGAGCGGAGCGCTTGTCTATCCGACCTTTG	1140
Qy	1141	CAGTGGCTTTATGTGCTGGAATTAATTTGGGCTGTCAAGCCGATGGAATGAAATGAG	1200
Db	1141	CAGTGGCTTTATGTGCTGGAATTAATTTGGGCTGTCAAGCCGATGGAATGAAATGAG	1200
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Db	1201	TGATGAGGCAAGATTTCTTTGAGCAGAAATCAACATTTAGTGAATGAAATCTTCGATC	1260
Qy	1261	CTTACCTGATTAATTTGGCTATCTCTTCTGAAGAAATTTGGTGCCACCAAGGTTTAA	1320
Db	1261	CTTACCTGATTAATTTGGCTATCTCTTCTGAAGAAATTTGGTGCCACCAAGGTTTAA	1320
Qy	1321	TGCAAGCGTGCAGGTTCAAGAGAGAGCTTGGATTAATCTTATTTGCAACAACA	1380
Db	1321	TGCAAGCGTGCAGGTTCTCTCTGCTACCTGATGATTTGTTGGTGCAACAAGCAG	1380
Db	1381	CTGCAATCCCAAGGTTAAAGAGAGATTTAACTGTATATGCAATTAACCTCATACAG	1440
Qy	1441	TCACCAAGTACTTGGCTTACCTATCTTTTCTAACAAGAGAGGATTAATACCTTTC	1500
Db	1441	TCACCAAGTACTTGGCTTACCTATCTTTTCTAACAAGAGAGGATTAATACCTTTC	1500
Qy	1501	TAAAGCTTTGGGACTCATGATTAATTTTCAAAATCTGTCCAATGATGCTTAATC	1560
Db	1501	TAAAGCTTTGGGACTCATGATTAATTTTCAAAATCTGTCCAATGATGCTTAATC	1560
Qy	1561	TAAAGTGTGATGATCAAACTTGCACCTTTAATGAAAAAAGCTTCCGGCCAGAA	1620
Db	1561	TAAAGTGTGATGATCAAACTTGCACCTTTAATGAAAAAAGCTTCCGGCCAGAA	1620
Qy	1621	GTTCACTGGGCTTGCAGCTTTCTCATATATGTTTTTGTGATTAAGAAATGCCAAAGTTG	1680
Db	1621	GTTCACTGGGCTTGCAGCTTTCTCATATATGTTTTTGTGATTAAGAAATGCCAAAGTTG	1680
Qy	1681	CTGCTTGCATCTGAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1721
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LOCUS			
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VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
ORIGIN			
Query Match			
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Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Qy	61	AGATGCTGTCGCTGGAAGCTGCGCTGCGCGCGCGCGCTGATGCTGCTCTGCGGCT	120
Db	61	AGATGCTGTCGCTGGAAGCTGCGCTGCGCGCGCGCGCTGATGCTGCTCTGCGGCT	120
Qy	121	CGCTGGGTCCTCTCTCCCTGCGGCGCTGCGCGAGCTGCGAAGCAAGACAGAGCTGTGG	180
Db	121	CGCTGGGTCCTCTCTCCCTGCGGCGCTGCGCGAGCTGCGAAGCAAGACAGAGCTGTGG	180
Qy	181	ACCTGACCTTCTTACCCAGAGCGGCTGACCTGTGAGCCCTGCTGCTGCTGCTGCTA	240
Db	181	ACCTGACCTTCTTACCCAGAGCGGCTGACCTGTGAGCCCTGCTGCTGCTGCTGCTA	240
Qy	241	CCATTGAGCCAACTGCGCAGGAGCCGCGGCTTCTCATCTCTGCGGTTCTCCAAAGC	300
Db	241	CCATTGAGCCAACTGCGCAGGAGCCGCGGCTTCTCATCTCTGCGGTTCTCCAAAGC	300
Qy	301	TTTGATCTTGGCCAGAGGCTTGTCTCTGCTGATCTGAGGTTGGTGCCACCAAGACAG	360

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Db      ||| 301 TTGCACTTGGCCAGAGGCTGTCTCTCGCTACCTGAGGTTGGTGGCAACGACAG 360
Qy      ||| 361 ACTTCCTAATTTTGGATCCCAAGAAAGATCACTTTGAAGAGAAAGTTACCTGGCAAT 420
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Qy      ||| 421 CTCAAGTCAACCAAGATATTGGCAAAATATGGATCCATCCCTCTGATGGAGGAGAGT 480
Db      ||| 421 CTCAAGTCAACCAAGATATTGGCAAAATATGGATCCATCCCTCTGATGGAGGAGAGT 480
Qy      ||| 481 TACGGTTGAATGGCCCTACCAAGAGCAATGCTACTCCAGAAACACTACCAAGAAAAGT 540
Db      ||| 481 TACGGTTGAATGGCCCTACCAAGAGCAATGCTACTCCAGAAACACTACCAAGAAAAGT 540
Qy      ||| 541 TCAAGAACAGCACTTCAAGAAAGCTCTGATGATGCTATACCTTTGCAAACTGCT 600
Db      ||| 541 TCAAGAACAGCACTTCAAGAAAGCTCTGATGATGCTATACCTTTGCAAACTGCT 600
Qy      ||| 601 CAGGACTGGAATTGATCTTGGCTTAAATGGCTTATTAAGAACAGCAAGATTGGCAGTGA 660
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Qy      ||| 721 GGGAACTGAGCAATGAACCTTAACAGTTCTTAAAGAGGCTGATTTTCACTCAATGGGT 780
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Qy      ||| 781 CGCAGTTAGAGAGATTAATTAATCAATGCACTAACTCTAAGAAAGTCCACTTCAAAA 840
Db      ||| 781 CGCAGTTAGAGAGATTAATTAATCAATGCACTAACTCTAAGAAAGTCCACTTCAAAA 840
Qy      ||| 841 ATGCAAAACCTATGCTCTGATGTTGCTGACCTCGAAGAAAGACGCTTAAGATGCTGA 900
Db      ||| 841 ATGCAAAACCTATGCTCTGATGTTGCTGACCTCGAAGAAAGACGCTTAAGATGCTGA 900
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Qy      ||| 961 TGAATGAGCGAGCTGCTACACGAGGAAAGATTTCTAACCCTGATGATTTGCAATTTT 1020
Db      ||| 961 TGAATGAGCGAGCTGCTACACGAGGAAAGATTTCTAACCCTGATGATTTGCAATTTT 1020
Qy      ||| 1021 TTTGATCTGTGCAAAAAGTTTTCAGAGTGTGAGAGCAACGAGCTGGCAAGAGGTCT 1080
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Qy      ||| 1141 CAGCGGCTTTATGCTGAGATAAATTGGGCTGTACCGCGAATGGGAAATAGAAAGTG 1200
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Qy      ||| 1501 TAAGACCTTTGGGACCTCATGATTAATTCCAATCTGTCCAACTCAATGTTCTAACTC 1560
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Db      ||| 1561 TAAAGATGATGATGATCAAACTTCCGACCTTTAATGAGAAAACCTCTCCGGCAGAGAA 1620
Qy      ||| 1621 GTTCACCTGGGCTTGCACCTTCTCATATAGTTTCTTGTGATTAAGAAATGCCAAAGTTG 1680
Db      ||| 1621 GTTCACCTGGGCTTGCACCTTCTCATATAGTTTCTTGTGATTAAGAAATGCCAAAGTTG 1680
Qy      ||| 1681 CTGCTTCATCTGAAAATTAATATATATAGTCTGACACTG 1721
Db      ||| 1681 CTGCTTCATCTGAAAATTAATATATATAGTCTGACACTG 1721

RESULT 3
ARI25603 1721 bp. DNA linear PAT 16-MAY-2001
LOCUS Sequence 1 from patent US 6177545.
ACCESSION ARI25603 GI:14111665
VERSION ARI25603.1
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1721)
AUTHORS Pecker, I., Vlodevsky, I., Friedman, Y. and Perets, T.
TITLE Hepatocellular carcinoma specific molecular probes and their use in research and
JOURNAL medical applications
PATENT: US 6177545-A 1 23-JAN-2001;
FEATURES
location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 1721; DB 6; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1721; Conservative 0;

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Db      ||| 61 AGATGCTGCTGCTGCAAGCTGCGCTGCGCGCGCTGATGCTGCTCTGGGGC 120
Qy      ||| 61 AGATGCTGCTGCTGCAAGCTGCGCTGCGCGCGCTGATGCTGCTCTGGGGC 120
Db      ||| 61 AGATGCTGCTGCTGCAAGCTGCGCTGCGCGCGCTGATGCTGCTCTGGGGC 120
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Db      ||| 121 CGCTGGGTCCTCTCCCTGCGCGCGCTGCGCGCGAGCTGCGAGCAAGACAGGACGTCG 180
Qy      ||| 181 ACTGGAATCTTCAACCAAGAGCGGTGCACTGATGAGCCCTGTTCTGTCCTGCA 240
Db      ||| 181 ACTGGAATCTTCAACCAAGAGCGGTGCACTGATGAGCCCTGTTCTGTCCTGCA 240
Qy      ||| 241 CCATTGACGCAACCTGCGCAGGACCGCGGTTCTCATCTCTGGGTTCTCAAAAGC 300
Db      ||| 241 CCATTGACGCAACCTGCGCAGGACCGCGGTTCTCATCTCTGGGTTCTCAAAAGC 300
Qy      ||| 301 TTGTTACCTTGGGCAAGAGGCTGCTCTGCTGCTGCTGAGGTTTGGTGGCAAGACAG 360
Db      ||| 301 TTGTTACCTTGGGCAAGAGGCTGCTCTGCTGCTGCTGAGGTTTGGTGGCAAGACAG 360
Qy      ||| 361 ACTTCCTAATTTTGGATCCCAAGAAAGATCACTTTGAAGAGAGATTAACCTGCAAT 420

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Db 361 ACTTCCTAATTTTGCATCCCAAGAGAAATCAACCTTTGAGAGAGAGATTAATCTGCAAT 420
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Db 1621 GTTACCTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATPAGAAATGCCAAAGTTG 1680
Qy 1681 CTGCTGCATCTGAAATTAATAATATAGTACTAGTCTGACACTG 1721
Db 1681 CTGCTGCATCTGAAATTAATAATATAGTACTGCTGACACTG 1721

RESULT 4
ARI25604 1721 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 3 from patent US 6177545.
DEFINITION ARI25604
ACCESSION ARI25604.1 GI:14111666
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 1721)
Pecker, I., Vlodavsky, I., Friedman, Y. and Peretz, T.
Heparanase specific molecular probes and their use in research and
medical applications
Patent: US 6177545-A 3 23-JAN-2001;
JOURNAL Location/Qualifiers
FEATURES
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1..1721
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 1721; DB 6; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 181 ACCTGGAATTTCTTCAACCGAGAGCGGCTGCACTGATGAGCGCCCTCTCTCTGTCCTCA 240
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Qy 241 CCAATTGACGCAACCTGCGCAACCGAGCGGCTTCTCATCTCTCTGAGTTCTTCAAGC 300
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Db 361 ACTTCCTAATTTTGCATCCCAAGAGAGATCAACCTTTGAAGAGAGAGATTAATCTGCAAT 420
Qy 421 CTGAAGCAACCGAGATATTGGCAATATGATATCCATCCCTCTGATGTGAGAGAGAT 480

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Db	481	TAAGGTTGGAAATGACCCTACACAGAGCAATGCTACTCCGAGAACATCAACAGAAAAAGT	540
Oy	541	TCMAAGAACAGCACTTAAGAGAGCTGTGATGTGCTATACACTTTTGCAAACTGCT	600
Db	541	TCMAAGAACAGCACTTAAGAGAGCTGTGATGTGCTATACACTTTTGCAAACTGCT	600
Oy	601	CAGGACTGGAAGCTTGAATCTTGGCTTAAAGCGTATTTAAGAAAGAGATTTGCAGTGA	660
Db	601	CAGGACTGGAAGCTTGAATCTTGGCTTAAAGCGTATTTAAGAAAGAGATTTGCAGTGA	660
Oy	661	ACAGTTCTAATGCTCAGTTGCTCCTGGAAGTACTGCTCTTCCAGGGGTATTAACATTCTT	720
Db	661	ACAGTTCTAATGCTCAGTTGCTCCTGGAAGTACTGCTCTTCCAGGGGTATTAACATTCTT	720
Oy	721	GGGAAGTACGCAATGAACTTAACAGTTTCTTAAGAAAGCTGATTTTCATCAATGGGT	780
Db	721	GGGAAGTACGCAATGAACTTAACAGTTTCTTAAGAAAGCTGATTTTCATCAATGGGT	780
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Db	841	ATGCAAAACCTATATGCTGCTGATGTTGTCACGCTCGAAGAAAGAGGCTTAAGATCTGA	900
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Db	901	AGAGCTTCTGAAGGCTGTGTGAGAAAGTATGATTCAATTACATGAGCATCACTACTATT	960
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Db	1021	TTTCACTGTGTGCAAAAAGTTTTCAGATGGTTGAGAGACACAGGCTGTGCAAGAGGCTC	1080
Oy	1081	GGTTAGAGAGAAACAGCTGTGCATATGAGAGCGAGCGCCTTTGCTATCCGACACCTTTG	1140
Db	1081	GGTTAGAGAGAAACAGCTGTGCATATGAGAGCGAGCGCCTTTGCTATCCGACACCTTTG	1140
Oy	1141	CAGCTGTGCTTATGTGTGCTGTGATTAATTTGGGCTGTCAAGCCGAAATGGGAATGAAGTGG	1200
Db	1141	CAGCTGTGCTTATGTGTGCTGTGATTAATTTGGGCTGTCAAGCCGAAATGGGAATGAAGTGG	1200
Oy	1201	TGATGAGGCAAGATATCTTTGAGACAGAAACATCACTTATAGTGAATGAATACTTGATC	1260
Db	1201	TGATGAGGCAAGATATCTTTGAGACAGAAACATCACTTATAGTGAATGAATACTTGATC	1260
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Db	1261	CTTAACTGATTAATTTGGCTATCTCTTCTGTCAAGAAATTTGGTGGCCACCAAGGTGTAA	1320
Oy	1321	TGGCAAGCGTGTCAAGGTTCAAGAGAGAGAGCTTGAAGTATACCTTCATTGCAACAA	1380
Db	1321	TGGCAAGCGTGTCAAGGTTCAAGAGAGAGAGCTTGAAGTATACCTTCATTGCAACAA	1380
Oy	1381	CTGACAAATCAAGGTTAATAAGAGAGATTTAACTGTATGCAATTAACCTGCATPAAG	1440
Db	1381	CTGACAAATCAAGGTTAATAAGAGAGATTTAACTGTATGCAATTAACCTGCATPAAG	1440
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DB	1501	TAAAGACCTTTGGGACCTTCAGATGATTACTTTCGAAATCTGTCCAACTGATGCTTAATCTC	1500		
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DB	1561	TAAAGATGATGATGATGATCAAACTTGGCCACTTTAATGAAAAAGCTTCGCGCCAGAA	1620		
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DB	1621	GTTCACTGGGGCTTCCGAGCTTTCATATAGTTTTTTTGATAGAAAGGCCAAAGTTG	1680		
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LOCUS	BD193236				
DEFINITION	Heparamase specific molecular probes and their use in research and medical applications.				
ACCESSION	BD193236				
VERSION	BD193236.1				
KEYWORDS	JP 2002512533-A/1.				
SOURCE	Streptococcus equi				
ORGANISM	Streptococcus equi				
REFERENCE	Bacteriia; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.				
AUTHORS	1 (bases 1 to 1721)				
TITLE	Pecker,I., Vlodavsky,I., Friedman,Y. and Perets,T.				
JOURNAL	Heparamase specific molecular probes and their use in research and medical applications				
COMMENT	Patent: JP 2002512533-A 1 23-APR-2002; INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES & DEVELOPMENT LTD				
PN	JP 2002512533-A/1				
PD	23-APR-2002				
PF	29-APR-1999				
PR	01-MAY-1998				
PI	IRIS PECKER,ISRAEL VLODAVSKY,YAEL FRIEDMAN,TUVIA PERETS PC				
C07K16/00,C07K16/40,G01N33/53,C07H21/02,CTH21/04,A61K39/395 CC					
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FEATURES	key	Location/Qualifiers.			
source	1..1721	Location/Qualifiers			
ORIGIN	1..1721	Location/Qualifiers			
Query Match	100.0%; Score 1721; DB 6; Length 1721;				
Best local similarity	100.0%; Pred. No. 0;				
Matches 1721; Conservative	0; Mismatches	0; Indels	0; Gaps	0;	
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DB	61	AGATGCTGCTGCGCTCGAAGCTCGCTGCGCGCCGCGCTGATGCTGCTCTCTGGAGC	120		
QY	121	CGCTGGGCTCCCTCTCCCTCGGCGCCTGCGCCGAGCACTGGCGCAAGCAAGAAGTCTG	180		
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QY	181	ACCTGACTTTTCAACCCAGAGCCGCTGCACTGGTAGGCCCTGTTCTGTGCGTCA	240		
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QY	241	CCATTGACGCAACCTTGCCACCGAGCCCGGGGTTCCATCTCTGGTTTCCCAAGC	300		
DB	241	CCATTGACGCAACCTTGCCACCGAGCCCGGGGTTCCATCTCTGGTTTCCCAAGC	300		

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 LOCUS
 DEFINITION Cells genetically modified for expressing recombinant heparanase
 ACCESSION BD205238
 VERSION BD205238.1 GI:33015008
 KEYWORDS JP 2002513560-A/1.
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 1721)
 AUTHORS Artzi,H.B., Herzhkovitz,M.A., Zeevi,O.Y., Pecker,I., Peleg,Y., Shlom,Y., Moskowicz,H., Miron,D., Gilboa,A. and Miron,M.
 Cells genetically modified for expressing recombinant heparanase and method, and method of purifying recombinant heparanase
 Patent: JP 2002513560-A 1 14-MAY-2002;
 INSIGHT STRATEGY AND MARKETING LTD
 JOURNAL OS Unidentified
 COMMENT
 PN JP 2002513560-A/1
 PD 14-MAY-2002
 PF 29-APR-1999 JP 2000547200
 PR 01-MAY-1998 US 09/071618 02-MAR-1999 US 09/260038 PI
 HANNA BEN ARTZI,MATY AYAL HERSHKOVITZ,ORON YACOBY ZEEVI,IRIS PECKER,
 PI YOAV PELEG,YINON SHLOMI,HAIM MOSKOWITZ,DEPHNA MIRON,AYELEF PI
 GILBOA,
 PI MADELENE MIRON
 PC C12N15/09,C07K16/40,C12N1/19,C12N1/21,C12N5/10,C12N9/24,C12N15/ PC
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 CC Strandedness: Double;
 CC Topology: Linear;
 CC Cells genetically modified for expressing recombinant CC
 heparanase and
 CC method, and method of purifying recombinant heparanase. FH
 Key source Location/Qualifiers
 FT 1..1721
 FT /organism='Unidentified'.

FEATURES
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 Location/Qualifiers
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Query Match 100.0%; Score 1721; DB 6; Length 1721;
 Best Local Similarity 100.0%; Pred. No. 0;
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1 CTAGAGCTTTCGATCTCCCGCTGCGGCGGAGCTGCGGCGGAGAGCCAGGTGAGCCCA 60
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RESULT 8
 BD05239 1721 bp DNA linear PART 17-JUL-2003
 LOCUS Cells genetically modified for expressing recombinant heparanase
 DEFINITION and method of purifying recombinant heparanase.
 ACCESSION BD05239 GI:33015009
 VERSION JP 2002513560-A/2.
 KEYWORDS unclassified
 SOURCE ORGANISM
 unclassified.
 REFERENCE 1 (bases 1 to 1721)
 AUTHORS Artzi, H.B., Hershkowitz, M.A., Zeevi, O.Y., Pecker, I., Peleg, Y., Shlom, Y., Moskowicz, H., Miron, D., Gilboa, A. and Miron, M.
 TITLE Cells genetically modified for expressing recombinant heparanase and method of purifying recombinant heparanase
 JOURNAL Patent: JP 2002513560-A 2 14-MAY-2002;
 INSIGHT STRATEGY AND MARKETING LTD

COMMENT OS Unidentified
PN JP 2002513560-A/2
14-MAY-2002
29-APR-1999 JP 2000547200
01-MAY-1998 US 09/071618.02-MAR-1999 US 09/260038 PI
HANNA BEN ARTZI, WATY AYAL, HERSHKOVITZ, ORON YACOB, ZEEVI, IRIS
PECKER,
PI YOAV PELEG, YINON SHLOMI, HAIM MOSKOWITZ, DEPHNA MIRON, AYELET
GILBOA,
PI MADELENE MIRON
PC
C12N15/09, C07K16/40, C12N1/19, C12N1/21, C12N5/10, C12N9/24, C12N15/ PC
00, C12N5/00
CC Topology: linear;
CC Cells genetically modified for expressing recombinant CC
heparanase and
CC method, and method of purifying recombinant heparanase. FH
Key Location/Qualifiers
FT source 1.1721
PI Location/Qualifiers
1.1721
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ORIGIN

Query Match 100.0%; Score 1721; DB 6; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 GCGTGGGCTCCCTCCCTCCGCGCGCCGCGCGCACTGCGCAAGAGAGAGAGAGAGAG 180
DB 121 GCGTGGGCTCCCTCCCTCCGCGCGCCGCGCGCACTGCGCAAGAGAGAGAGAGAGAG 180
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DB 541 TCAAG 600
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DB 601 CAGAGCTGAGCTTGAATCTTTGGCTTAAATGCGTTATTAAGAGAGAGAGAGAGAGAG 660
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RESULT 9				
LOCUS	AR194189			
DEFINITION	AR194189	1721 bp	DNA	
ACCESSION	Sequence 1 from patent US 6348344.		linear	PAT 20-APR-2002
VERSION	AR194189			
KEYWORDS	AR194189.1	GI:20240781		
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 1721)			
TITLE	Ayal-HersHKovitz, M., Moskowicz, H., Miron, D., Gilboa, A., Mimoun, M., Ben-Atzi, H., Yacoby-Zeevi, O., Becker, I., Peleg, Y., and Schiomi, Y. Genetically modified cells and methods for expressing recombinant hapatemase and methods of purifying same			
JOURNAL	Patent: US 6348344-A 1 19-FEB-2002;			
FEATURES	Location/Qualifiers			
SOURCE	1..1721			

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ORIGIN

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Query Match	100.0%	Score 1721;	DB 6;	Length 1721;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1721; Conservative	0;	Mismatches	0;	T-1-1-

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OY	61	AGATGCTGTCGCGCTCGAAGCTGCGCGTCGCGCGCGCGCTGATGCTGCTGCTCTGGGGC	120
Db	61	AGATGCTGTCGCGCTCGAAGCTGCGCGCTGCGCGCGCTGATGCTGCTGCTCTGGGGC	120
OY	121	CGCTGGGTCGCCCTCTCCCTCGGCGCTCTGCCCGACCTGCGCAGACAGAGACGTCTGG	180
Db	121	CGCTGGGTCGCCCTCTCCCTCGGCGCTCTGCCCGACCTGCGCAGACAGAGACGTCTGG	180
OY	181	ACCTGGACTTCTTCAACCCAGAGCGCGCTGACCTGATGAGCCCTCGTCTCTGTCCTCA	240
Db	181	ACCTGGACTTCTTCAACCCAGAGCGCGCTGACCTGATGAGCCCTCGTCTCTGTCCTCA	240
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Db	241	CCATTGAGCGCCAACTGCGCCACGAGACCCGCGGTTCTCATCTCTCGTGGTTCTCCAAAGC	300
OY	301	TTCTGACTTGCGCCAGAGCTTGATCTCTCGTGATACCTGAGGTTTGGTGACCAAGAC	360
Db	301	TTCTGACTTGCGCCAGAGCTTGATCTCTCGTGATACCTGAGGTTTGGTGACCAAGAC	360
OY	361	ACTTCCTAATTTTGGATCCCAAGAGGAAATCACTTTGAAAGAGAGATTACTGCGCAAT	420
Db	361	ACTTCCTAATTTTGGATCCCAAGAGGAAATCACTTTGAAAGAGAGATTACTGCGCAAT	420
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Db	421	CTCAAGTCACACAGAAATTTTGCAAAATATGGAATCAATCCCTCGATATGTGAGAGAAAT	480
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Db	481	TAGGGTTGGAATGGCCCTCACAGAGCAATTGTCTACTCCGAGAACTACAGAAAAAT	540
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Db	541	TCAAGAACACACTACTCAAGAAGCTCTGTATATGCTATACATTTTGGAACTGCT	600
OY	601	CAGAGCTGGACTTGATCTTTGGCTTAAATGCGTTATTAAGAACAGCAGATTGCACTGGA	660
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D	781	CGCACTTAGGGAGAGATTATTAATTCATATTCATTAACCTTCTTAAGAAAGTCGACCTTCAAA	840
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Q	1681	CTGCTTGCATCTGAATAATAAATATATCTAATGCTTCAACCTG	1721
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RESULT 10

ACCESSION AR221285
VERSION AR221285.1 GI:23328256
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1721) Pecker, I. and Yacoby-Zeevi, O.
AUTHORS Harel-Herskovitz, M.,
TITLE Genetically modified cells and methods for expressing recombinant
heparanase and methods of purifying same
JOURNAL Patent: US 6426209-A 1 30-JUL-2002;
FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 1721; DB 6; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AR221286 1721 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 3 from patent US 6426209.
ACCESSION AR221286
VERSION AR221286.1 GI:23328257
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1721)
AUTHORS Ayal-HersHKovltz,M., Pecker,I. and Yacoby-Zeevi,O.
TITLE Genetically modified cells and methods for expressing recombinant
heparanase and methods of purifying same
JOURNAL Patent: US 6426209-A 3 30-JUL-2002;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

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Query Match 100.0%; Score 1721; DB 6; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 1 from patent US 6475763.
ACCESSION AR243203
VERSION AR243203.1 GI:27290318
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1721)
AUTHORS Ayal-HersHKovltz,M., Moskowltz,H., Miron,D., Gilboa,A., Mimon,M.,

TITLE Ben-Artzi, H., Yacoby-Zeevi, O., Pecker, I., Peleg, Y. and Shlom, Y.
Genetically modified cells and methods for expressing recombinant
heparanase and methods of purifying same
JOURNAL Patent: US 645763-A 1 05-NOV-2002;
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RESULT 14
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SEQUENCE 3 from patent US 645763.
AR243204
AR243204.1 GI:27290319
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
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AUTHORS
Ben-Artzi, H., Yacoby-Zeevi, O., Pecker, I., Peleg, Y. and Shlom, Y.
TITLE
Genetically modified cells and methods for expressing recombinant
heparanase and methods of purifying same

JOURNAL Patent: US 6475763-A 3 05-NOV-2002;
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ACCESSION AR287435
VERSION AR287435.1 GI:29725129
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1721)
AUTHORS Pecker,I., Vlodavsky,I., Friedman,Y. and Perets,T.
TITLE Hepatocarcinoma specific molecular probes and their use in research and medical applications
JOURNAL Patent: US 6531129-A 1 11-MAR-2003;
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Query Match 100.0%; Score 1721; DB 6; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
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Db	181	ACCTGGAATCTTCTCAACCAAGAGCCGCTGCACTGCTGAGCCCTGCTGCTGCTCA	240
QY	241	CCATTGACGCAACCTGCGCAACGACCCGCTGCTCACTGCTGAGCTTCCCAAGC	300
Db	241	CCATTGACGCAACCTGCGCAACGACCCGCTGCTCACTGCTGAGCTTCCCAAGC	300
QY	301	TTCCGACCTTGGCCAGAGGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360
Db	301	TTCCGACCTTGGCCAGAGGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	360
QY	361	ACTTCTTAATTTTGCATCCCAAGAGATCAACCTTGAAGAGAGAGTTCCTGGCAAT	420
Db	361	ACTTCTTAATTTTGCATCCCAAGAGATCAACCTTGAAGAGAGTTCCTGGCAAT	420
QY	421	CTCAAGTCAACAGAGATTTTGCATATGATTCATCCCTGCTGATGCTGAGAGAGT	480
Db	421	CTCAAGTCAACAGAGATTTTGCATATGATTCATCCCTGCTGATGCTGAGAGAGT	480
QY	481	TACGGTTGAATGCGCTTACCAAGAGCAATTTGCTACCTGCAAGAGCACTACGAAAGT	540
Db	481	TACGGTTGAATGCGCTTACCAAGAGCAATTTGCTACCTGCAAGAGCACTACGAAAGT	540
QY	541	TCAGAAACGCACTTCTCAAGAGCTCTGATGATGCTGCTGCTGCTGCTGCTGCTG	600
Db	541	TCAGAAACGCACTTCTCAAGAGCTCTGATGATGCTGCTGCTGCTGCTGCTGCTG	600
QY	601	CAGACTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660
Db	601	CAGACTGCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	660
QY	661	ACAGTTCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	720
Db	661	ACAGTTCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	720
QY	721	GGGAACTAGGCAATGCACTTCAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTG	780
Db	721	GGGAACTAGGCAATGCACTTCAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTG	780
QY	781	CGCACTTAGGCAATGCACTTCAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTG	840
Db	781	CGCACTTAGGCAATGCACTTCAAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTG	840
QY	841	ATGCAAACTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900
Db	841	ATGCAAACTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900
QY	901	AGAGCTTCTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960
Db	901	AGAGCTTCTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	960
QY	961	TGAATGACGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1020
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QY	1021	TTTCATCTGCTGCAAAAGTTTTCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1080
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Db	1081	GGTTAGGAAACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1140
QY	1141	CAGCTGGCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1200
Db	1141	CAGCTGGCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1200
QY	1201	TGATGAGGCAAGTATTTCTTGGAGCAAGAACTCACTTATGATGATGAAATCTTGATC	1260
Db	1201	TGATGAGGCAAGTATTTCTTGGAGCAAGAACTCACTTATGATGATGAAATCTTGATC	1260
QY	1261	CTTTCACGATTAATTTGGCTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1320
Db	1261	CTTTCACGATTAATTTGGCTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1320
QY	1321	TGGCAAGCTGCAAGTTCGAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1380
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QY	1381	CTGCAATCCAGATTAATGAAAGAGATTTAACTGATGCAATTAATCTTCAATGAG	1440
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QY	1441	TCACCAAGTACTGCGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1500
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QY	1681	CTGCT 1685	
Db	1681	CTGCT 1685	
RESULT 2			
LOCUS			
CR610536			
DEFINITION			
full-length cDNA clone CSOD1028YF04 of Placenta Cot 25-normalized			
ACCESSION			
CR610536			
VERSION			
CR610536.1 GI:50491343			
KEYWORDS			
HTC; cDNA.			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
REFERENCE			
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
AUTHORS			
L.M.B., Gruber, C., Jessee, J., and Polayes, D.			
TITLE			
Full-length cDNA libraries and normalization			
JOURNAL			
Unpublished			
REMARK			
Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600			
Paradey Avenue			
2 (bases 1 to 1665)			
REFERENCE			
Genoscope.			
AUTHORS			
Direct Submission			
TITLE			
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :			
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqrefgenoscope.cns.fr			
- Web : www.genoscope.cns.fr)			
COMMENT			
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime			
end enriched, double-strand cDNA was digested with NotI and cloned			
into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library			
was normalized. Library was constructed by Life Technologies, a			
division of Invitrogen.			
FEATURES			
Location/Qualifiers			
1..1665			

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1028YF04"
/issue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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ORIGIN

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Query Match      96.0%; Score 1651.6; DB 3; Length 1665;
Beet Local Similarity 99.8%; Pred. No. 0;
Matches 1654; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 1 CTAGAGCTTTCGACTCTCCGCTGCGCGAGCTGGCGGGGAGGAGCGAGCTGAGCCCA 60
DB 8 CTAGAGCTCTGACCTCTCCGCTGCGCGAGCTGGCGGGGAGGAGCGAGCTGAGCCCA 67
QY 61 AGATCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTCTCTGGGAGC 120
DB 68 AGATCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCGCTGATGCTGCTCTCTGGGAGC 127
QY 121 CGCTGGGTCCTCTCCCTGCGCGCTGCGCGCGCGAGCTGGCGAGCAGACAGACGTCGTGG 180
DB 128 CGCTGGGTCCTCTCCCTGCGCGCTGCGCGCGCGAGCTGGCGAGCAGACAGACGTCGTGG 187
QY 181 ACCTGGAATCTTCAACCGAGAGCGCTGCACTGTGAGCCCTCTGTTCTGTCCGTCA 240
DB 188 ACCTGGAATCTTCAACCGAGAGCGCTGCACTGTGAGCCCTCTGTTCTGTCCGTCA 247
QY 241 CCATTGAGCGCAACCTGGCGAGAGCCGCGGTTCTCTATCTCTGAGTTCTCCAAAGC 300
DB 248 CCATTGAGCGCAACCTGGCGAGAGCCGCGGTTCTCTATCTCTGAGTTCTCCAAAGC 307
QY 301 TTTCGTAACCTGGCGAGAGCTGTCTCTGCTGCTACTGAGTTGTGTGGACCAAGAGAG 360
DB 308 TTTCGTAACCTGGCGAGAGCTGTCTCTGCTGCTACTGAGTTGTGTGGACCAAGAGAG 367
QY 361 ACTTCTTAATTTTCGATCCCAAGAGAGATCAACTTTGAAGAGAGATTACTGGCAAT 420
DB 368 ACTTCTTAATTTTCGATCCCAAGAGAGATCAACTTTGAAGAGAGATTACTGGCAAT 427
QY 421 CTCAAGTCAACCAAGAGATTTTTCGAAATATGATTCATCTCTGATGTGAGAGAAAGT 480
DB 428 CTCAAGTCAACCAAGAGATTTTTCGAAATATGATTCATCTCTGATGTGAGAGAAAGT 487
QY 481 TACGGTTGGAATGCGCCCTTACCAAGAGCAATTTGCTACTCCGAGAACATCAACCGAAAGT 540
DB 488 TACGGTTGGAATGCGCCCTTACCAAGAGCAATTTGCTACTCCGAGAACATCAACCGAAAGT 547
QY 541 TCAAGAACAGCACTACTCAAGAGAGCTGTATGATGTGCTATACACTTTTGGCAACTGCT 600
DB 548 TCAAGAACAGCACTACTCAAGAGAGCTGTATGATGTGCTATACACTTTTGGCAACTGCT 607
QY 601 CAGGACTGAGCTTGATCTTTTGGCTTAAATGCGTTATTAAGAAACAGCAATTTTGAAGTGA 660
DB 608 CAGGACTGAGCTTGATCTTTTGGCTTAAATGCGTTATTAAGAAACAGCAATTTTGAAGTGA 667
QY 661 ACAAGTTCTTAATGCTCAAGTTGCTCTGAGACTACTGCTCTTCCAAAGGGGATTAACATTTTCT 720
DB 668 ACAAGTTCTTAATGCTCAAGTTGCTCTGAGACTACTGCTCTTCCAAAGGGGATTAACATTTTCT 727
QY 721 GGAAGCTAGGCAATGAACTTAACAGTTTCTTAAAGAGGCTGATATTTTTCATCAATGGGT 780
DB 728 GGAAGCTAGGCAATGAACTTAACAGTTTCTTAAAGAGGCTGATATTTTTCATCAATGGGT 787
QY 781 CGCAGTTAGAGAGATTAATATTCATATTCATTAACCTTTTAAAGAAAGTCCACTTTCAAAA 840
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DB 848 ATGCAAAACTCTAATGCTCTGATGTTGTGTCAGCCCTGGAAGAAAGCGGCTTAAGATGCTGA 907
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DB 968 TGAATGAGCGGACCTGCTACCAAGGAGAGATTTTCTTAAACCTCTGATGATTTGACATTTTGA 1027
QY 1021 TTTGATCTGTGCAAAAAGTTTTCAGGTTGTTGAGAGACCAAGGCTGGCAAGAGAGTCT 1080
DB 1028 TTTGATCTGTGCAAAAAGTTTTCAGGTTGTTGAGAGACCAAGGCTGGCAAGAGAGTCT 1087
QY 1081 GGTTAGAGAAACAAGCTCTGCTATATGAGAGCGGAGCGCCCTTCTATCCGACACTTTG 1140
DB 1088 GGTTAGAGAAACAAGCTCTGCTATATGAGAGCGGAGCGCCCTTCTATCCGACACTTTG 1147
QY 1141 CAGCTGCTTTATGCTGCTGATTAATTTGGCCCTGTAGCCCGGAATGGGAATAGAAGTGG 1200
DB 1148 CAGCTGCTTTATGCTGCTGATTAATTTGGCCCTGTAGCCCGGAATGGGAATAGAAGTGG 1207
QY 1201 TGATGAGCGCAAGTATTTCTTTGAGAGAGAACTACATTTAGTGAAGTGAATTCGATC 1260
DB 1208 TGATGAGCGCAAGTATTTCTTTGAGAGAGAACTACATTTAGTGAAGTGAATTCGATC 1267
QY 1261 CTTTACCTGATTAATTTGCTATCTCTTCTGTTCAAGAAATTTGTGGGCAACCAAGTGTAA 1320
DB 1268 CTTTACCTGATTAATTTGCTATCTCTTCTGTTCAAGAAATTTGTGGGCAACCAAGTGTAA 1327
QY 1321 TGGCAAGCTGTCAGAGTTTCAAGAGAGAGAGAGCTTCCAGTATACCTTCAATTCACAAACA 1380
DB 1328 TGGCAAGCTGTCAGAGTTTCAAGAGAGAGAGAGAGCTTCCAGTATACCTTCAATTCACAAACA 1387
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DB 1388 CTGACAAATCCAAAGGATTAAGAGAGAGATTAACCTGTATAGCATTAACCTCCATACG 1447
QY 1441 TCACCAAGTACTTTCGCTGCTTACCTTATCTTTTCTTAAACCAAGTGTATTAACCTTC 1500
DB 1448 TCACCAAGTACTTTCGCTGCTTACCTTATCTTTTCTTAAACCAAGTGTATTAACCTTC 1507
QY 1501 TAAAGCTTTTGGACCTCATGATGATTACTTTTCAAAATCTGTCCAACTCAATGCTTAATC 1560
DB 1508 TAAAGCTTTTGGACCTCATGATGATTACTTTTCAAAATCTGTCCAACTCAATGCTTAATC 1567
QY 1561 TAAAGATGTTGAGATGATCAAACTTGGCACTTTAATGAGAAACCTTCCGGCCAGGAA 1620
DB 1568 TAAAGATGTTGAGATGATCAAACTTGGCACTTTAATGAGAAACCTTCCGGCCAGGAA 1627
QY 1621 GTTCACTGGGCTTCCAGCTTTCTCATATAGTTTTTTT 1658
DB 1628 GTTCACTGGGCTTCCAGCTTTCTCATATAGTTTTTTT 1665
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RESULT 3
AK040471
LOCUS
DEFINITION Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
library, clone:A430101M04 product:hepatanase, full insert sequence.
ACCESSION AK040471.1 GI:26333764
VERSION AK040471.1
KEYWORDS HTC, CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
AUTHORS High-efficiency full-length cDNA cloning
TITLE Mech. Enzymol. 303, 19-44 (1999)
JOURNLS MEDLINE 99279253
PUBMED 10349636
REFERENCE
2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
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	TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)	
REFERENCE	6 (bases 1 to 1962)	
AUTHORS	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T., Horii,F., Imocani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Koike,Y., Kondo,S., Komoto,H., Kouda,M., Koye,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,K., Satoh,H., Sakai,C., Sakai,K., Sakazume,N., Sanjo,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Yuramatsu,M. and Hayashizaki,Y.	
TITLE	Direct Submission	
JOURNAL	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)	
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/ Location/Qualifiers	
SOURCE	1. 1962 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM DB:E030042C09" /db_xref="taxon:10090" /clone_id="E030042C09" /tissue_type="lung" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="0 day neonate" .1568 /note="heparanase (MGD MG1:134124, GB A047943, evidence: BLASTN, 99%, match=480) putative"	
ORIGIN	Query Match 54.2%; Score 933.4; DB 3; Length 1962; Best Local Similarly 78.7%; Pred. No. 1.5e-246; Matches 1152; Conservative 0; Mismatches 306; Indels 5; Gaps 3;	
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Qy 378 CCNAGAGAGATCAACCTTTGAGAGAGAGATTACTGGCAATCTCAAGTCACCAAGAT 437
Db 408 CCGAGCAAGAGAACCGACTTCGAGAGAGAGAGATTACTGGAATCTCAAGTCACCAAGAT 467
Qy 438 ATTGGCAAAATATGATCCATCCCTCTGATGTGAGAGAGAGATTACGGTTGGAATGAGCC 497
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Qy 558 TCAAGAGCTCTGATGATGTGATACATTTTGGCAACTGCTCAGAGCTGAGACTTGATC 617
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Db 828 TTTGGGAGATGTCATTAACCTTCTAAGAAAGTCCACCTTCAAAAATGCAAACTCTATGCT 887
Qy 858 CCTGATGTTGCTCAGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 917
Db 888 CCTGATGTTGCTCAGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCT 947
Qy 918 GATGAGAGAGATGATGATTCAGTTACATGAGCTACTACTATTTGAATGAGAGAGAGCT 977
Db 948 GCGGAGAGAGATGATGATTCAGTTACATGAGCTACTACTATTTGAATGAGAGAGAGCT 1007
Qy 978 ACNAGAGAGATTTCTAACCCTGATGATTTGAACATTTTATTTCAATCTGTGCAAAA 1037
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RESULT 6

AL552174

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

COMMENT

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Db      300 TTGTACTCTGGGCGACAGGCTTGTCTCTCGCGTAAGCTGAGTTGGTGCACCAAGACAG 359
Qy      361 ACTTCTTAATTTTTCGATGCCAAGAGATCAACCTTTAAGAGAGAAATTTCTGGCAAT 420
Db      360 ACTTCTTAATTTTTCGATGCCAAGAGATCAACCTTTAAGAGAGAAATTTCTGGCAAT 419
Qy      421 CTCATGACCAACAGATATTTGGCAATATGATATCCATCCCTCTGATGTGAGAGAAAGT 480
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Qy      481 TAGCGTTGAGATGGCCCTTACAGAGCATTTGCTCTCCGAGAACATTCACCAAAAGT 540
Db      480 TAGCGTTGAGATGGCCCTTACAGAGCATTTGCTCTCCGAGAACATTCACCAAAAGT 539
Qy      541 TCAGAGACAGCACTTACTCAGAGAGCTGTGATGTGATATACATTTTGGCAACTGCT 600
Db      540 TCAGAGACAGCACTTACTCAGAGAGCTGTGATGTGATATACATTTTGGCAACTGCT 599
Qy      601 CAGGACTGAGCTGATCTTTGGCCCTTAATGCGTTATTAAGAACAGCAATTTGCAATGGA 660
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Qy      661 ACAGTTCTAATGCTCAGTTGCTCTGAGACTACTGCTCTTCCAGAGGGGTATTAACATTTCTT 720
Db      660 ACAGTTCTAATGCTCAGTTGCTCTGAGACTACTGCTCTTCCAGAGGGGTATTAACATTTCTT 719
Qy      721 GGGAACTGAGCAATGAACCTTAACAGTTTCTTTAAGAGGCTGATATTTTCAATCAATGGGT 780
Db      720 GGGAACTGAGCAATGAACCTTAACAGTTTCTTTAAGAGGCTGATATTTTCAATCAATGGGT 779
Qy      781 CGCAGTTAGAGAGATTAATTAATGATGCAATTAACCTTTAAGAGAGCCCTTCAAAA 840
Db      780 CGCAGTTAGAGAGATTAATTAATGATGCAATTAACCTTTAAGAGAGCCCTTCAAAA 839
Qy      841 ATGCAAACTCTATGCTGCTGATGTGTGCTGAGCCTCGAAGAAAGACGGCTTAAGATGCTG- 899
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Qy      900 AAGAGCTTCTGAGAGGCTGTGAGAGAGTGAATTTGATTCATGATGATGATGATGATGAT 959
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Qy      960 TTGAATGACGG 971
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RESULT 7
AL545270 945 bp mRNA linear EST 25-MAR-2004
LOCUS DEFINITION AL545270 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION AL545270
VERSION AL545270.3 GI:45745753
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 945)
Li, W.B., Gruber, C., Jessee, J., and Polyes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:11267106.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2469.r

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?b=CS0D1028D020P1&c=2469.r>.
Location/Qualifiers
1. .945

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1028P04"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 52.4%; Score 902.6; DB 1; Length 945;
Best Local Similarity 99.3%; Pred. No. 3.9e-238;
Matches 916; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Qy      4 GAGCTTTCAGCTCTCCGCTGCGGCGAGCTGCGGGGAGAGCAGCCAGGTGAGCCCAAGA 63
Db      10 GGGATCTCGACTCTCCGCTGCGGCGAGCTGCGGGGAGAGCAGCCAGGTGAGCCCAAGA 69
Qy      64 TGTGCTGCGGCTGGAAGCTGCGGCTGCGGCGGCGGCGGCTGATATGCTGCTCTGGGCGCG 123
Db      70 TGTGCTGCGGCTGGAAGCTGCGGCTGCGGCGGCGGCGGCTGATATGCTGCTCTGGGCGCG 129
Qy      124 TGGGTCCTCTCTCCCTGCGGCGGCTGCGGCGGCGGCGGCTGATATGCTGCTCTGGGCGCG 183
Db      130 TGGGTCCTCTCTCCCTGCGGCGGCTGCGGCGGCGGCGGCTGATATGCTGCTCTGGGCGCG 189
Qy      184 TGGACTTCTTCAACCAAGAGCGGCTGCACTGTGTGAGCCCTCTGCTCTGCTGCTACCA 243
Db      190 TGGACTTCTTCAACCAAGAGCGGCTGCACTGTGTGAGCCCTCTGCTCTGCTGCTACCA 249
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Db      250 TTGAGGCCAAGCTGCGACAGACCGCGGTTCTGATCCTCTGAGGTTCTCCAAAGCTTC 309
Qy      304 GTACCTTGGCGAGGCTTGTCTCTGCGTACCTGAGGTTGTGTGACCAAGACAGACT 363
Db      310 GTACCTTGGCGAGGCTTGTCTCTGCGTACCTGAGGTTGTGTGACCAAGACAGACT 369
Qy      364 TCTTAATTTTCATCCCAAGAGAGATCAACCTTTGAAGAGAGATTAATGCGCAATCTC 423
Db      370 TCTTAATTTTCATCCCAAGAGAGATCAACCTTTGAAGAGAGATTAATGCGCAATCTC 429
Qy      424 AAGTCAACCGAGATATTTGCAATATGATGATCCTCTGATGTGAGAGAGAGTTAC 483
Db      430 AAGTCAACCGAGATATTTGCAATATGATGATCCTCTGATGTGAGAGAGAGTTAC 489
Qy      484 GGTGGAATGGCCCAACAGAGAGATTTGCTACTCCGAGAACATTAACCAAAAAGTTCA 543
Db      490 GGTGGAATGGCCCAACAGAGAGATTTGCTACTCCGAGAACATTAACCAAAAAGTTCA 549
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Db      610 GACTGGAATTGATCTTTGGCCTTAATGCTTATTAAGACAGAGATTTGAGTGAGACA 669
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	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Oy	AL545232/c	1027 bp mRNA linear	AL545232			Homo sapiens (human)		EST 25-MAR-2004				
			AL545232			Homo sapiens						
			AL545232			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.						
			AL545232.3			1.1 (bases 1 to 1027)						
			EST.			Li, W.B., Gruber, C., Jesssee, J., and Polayes, D.						
						Full-length cDNA libraries and normalization						
						Unpublished (2001)						
						On Feb 15, 2001 this sequence version replaced gi:31267068.						
Oy												
Db												
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Genoscope - Centre National de Séquençage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dG) primer. Five primers
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
2469.x
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?n=CS0D1028BC0C2NP1&c=2469.x>.

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FEATURES      Location/Qualifiers
source        1. .1027
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD10281F04"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN	Query Match	50.3%;	Score 866.4;	DB 1;	Length 1027;
	Best Local Similarity	97.3%;	Pred. No.4.3e-228;		
	Matches 870;	Conservative	9;	Indels 0;	Gaps 0;
Qy	765	ATTTCATCAATGGCTGCGAGTTAGAGAAATTAATTCATTGCATAACTTCTAAGA	824		
Db	894	ATATTTCATCAATGGCTGCGAGTTAGAGAAATTAATTCATTGCATAACTTCTAAGA	835		
Qy	825	AAGTCACCTTCAAAATAATGCAAACTCTATGGTCTCGATGTTGGTCAGCCTCGAAGAAG	884		
Db	834	AAGTCACCTTCAAAATAATGCAAACTCTATGGTCTCGATGTTGGTCAGCCTCGAAGAAG	775		
Qy	885	ACGGCTAAGATGCTGAGAGCTTCTCTGAAGCTGTGTGAGAAAGTATGATTCACTTACCA	944		

Db	774	ACGGCMAAATGCTGAAGAGCTTCTGAAGCGTGTGAGAAAGTATGATTGACTTACGTTACA	715
Qy	945	TGGCATCACTACTATTTTGAATGACGGACTGCTACACAGGAAAGTATTTCTTAAACCTGAT	1004
Db	714	TGGCATCACTACTATTTGMAATGACGGACTGCTACACAGGAAAGTATTAACCTAACCCTGAT	655
Qy	1005	GTATTTGGACATTTTATTTTTCATCTGTGCAAAAAGTTTCCAGGTGTGTGAGACACCAAG	1064
Db	654	GTATTTGGACATTTTATTTTTCATCTGTGCAAAAAGTTTCCAGGTGTGTGAGACACCAAG	595
Qy	1065	CTGTGGCAAGAGGTCTGGTTAGAGAAACAAGCTCTGCATATGAGAGCGAGCCGCTTG	1122
Db	594	CTGTGGCAAGAGGTCTGGTTAGAGAAACAAGCTCTGCATATGAGAGCGAGCGCCCTTG	535
Qy	1125	CTATCCGACACCTTTGGACGTGCGCTTTATGTGCTGTGATAAATTGGGCTGTACGCCGA	1184
Db	534	CTATCCGACACCTTTGGACGTGCGCTTTATGTGCTGTGATAAATTGGGCTGTACGCCGA	475
Qy	1185	ATGGGAAATGAGAGTGTGTATGAGGCAAGTATTTCTTTGGACGAGAACTACCATTTAGTG	1244
Db	474	ATGGGAATAGAAAGTGTGTATGAGGCAAGTATTTCTTTGGACGAGAACTACCATTTAGTG	415
Qy	1245	GATGAAAACTTGCATCCTTTACCTGATTTATGGCTATCTCTTCTGTTCAAGAAATTGCTG	1304
Db	414	GATGAAAACTTGCATCCTTTACCTGATTTATGGCTATCTCTTCTGTTCAAGAAATTGCTG	355
Qy	1305	GGCACCAAGGTGTTAATGGCAAGGCTCCAGGTTCAAAAGAAAGAGAGCTTCGAGTATAC	1364
Db	354	GGCACCAAGGTGTTAATGGCAAGGCTCCAGGTTCAAAAGAAAGAGAGAGCTTCGAGTATAC	295
Qy	1365	CTTCAATTGCACAACACTGACCAATCCCAAGATATTAAGAAGAGATTTTACTCTGATACC	1424
Db	294	CTTCAATTGCACAACACTGACCAATCCCAAGATATTAAGAAGAGATTTTACTCTGATACC	235
Qy	1425	ATPAAACCTCCATAACGTCACCAAGTACTTGGGTAAACCCTATTCCTTTTCTPACAGCAA	1484
Db	234	ATPAAACCTCCATAATGTCACCAAGTACTTGGGTAAACCCTATTCCTTTTCTPACAGCAA	175
Qy	1485	GTGATATAATACCTTTCTPAGACCTTTGGGACCTCATGTGATTACTTTCCAAATCTGTCCA	1544
Db	174	GTGATATAATACCTTTCTPAGACCTTTGGGACCTCATGTGATTACTTTCCAAATCTGTCCA	115
Qy	1545	CTCAATGTCATTAATCTTAAAGATGTGTGATGATCAAACTTTGCCACCTTTAATGGAATA	1604
Db	114	CTCAATGTCATTAATCTTAAAGATGTGTGATGATCAAACTTTGCCACCTTTAATGGAATA	55
Qy	1605	CCCTCCGGGACGAGAGTTCACTGGGGCTGGCACCTTCTCATATAGTTTTTTT 1658	
Db	54	CCCTCCGGGACGAGAGTTCACTGGGGCTGGCACCTTCTCATATATATTTTTTT 1	

RESULT 9
BX398409/c

LOCUS	1066 bp	mRNA	linear	EST 29-APR-2004
DEFINITION	BX398409 Homo sapiens PLAGENRA COT 25-NORMALIZED Homo sapiens CDNA clone CS001058Y124 3-PRIME, mRNA sequence.			
ACCESSION	BX398409			
VERSION	BX398409.2			
KEYWORDS	GI:46873668			
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1. (bases 1 to 1066)			
AUTHORS	Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.			
TITLE	Full-length cDNA libraries and normalization			
JOURNAL	Unpublished (2001)			
COMMENT	On May 13, 2003 this sequence version replaced gi:30617572.			
	Contact: Genoscope			
	Genoscope - Centre National de Sequencage			
	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE			
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			

Db	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Db	480	CTCAAGTCAACGAGATATTTGGCAAAATGGAATCCCTCCCTCGATGTGAGAGAGAGT	Bo691142	924 bp	mRNA	linear	EST 15-JUL-2002					
Qy	481	TACGGTTGATGGCCCTTACCAAGAGCAATGTGCTACTCCGAGAACCTACCAAAAAAGT	Bo691142	924 bp	mRNA	linear	EST 15-JUL-2002					
Db	540	TACGGTTGATGGCCCTTACCAAGAGCAATGTGCTACTCCGAGAACCTACCAAAAAAGT	Bo691142	924 bp	mRNA	linear	EST 15-JUL-2002					
Qy	541	TCAAGAACAGCACTTACTCAAGAAAGCTCTGTAGATGTCTATAACATTTTGCACCTGCT	Bo691142	924 bp	mRNA	linear	EST 15-JUL-2002					
Db	600	TCAAGAACAGCACTTACTCAAGAAAGCTCTGTAGATGTCTATAACATTTTGCACCTGCT	Bo691142	924 bp	mRNA	linear	EST 15-JUL-2002					
Qy	601	CAGAGCTGACCTGATCTTTGGGCTAAATGCGTATTAAGAACAGACGATTTGCACTGGA	Bo691142	924 bp	mRNA	linear	EST 15-JUL-2002					
Db	660	CAGAGCTGACCTGATCTTTGGGCTAAATGCGTATTAAGAACAGACGATTTGCACTGGA	Bo691142	924 bp	mRNA	linear	EST 15-JUL-2002					
Qy	661	ACAGTTCTAATGCTCAGTTGCTCTGAGCTACTGCTCTTCCAAAGGGTATTAACATTTCT	Bo691142	924 bp	mRNA	linear	EST 15-JUL-2002					
Db	720	ACATTTCTAATGCTCAGTTGCTCTGAGCTACTGCTCTTCCAAAGGGTATTAACATTTCT	Bo691142	924 bp	mRNA	linear	EST 15-JUL-2002					
Qy	721	GGGAATCTAGGCAATGAACCTAACAGATT--CTTTAAGAGCGTGATATTTTCATCAATGG	Bo691142	924 bp	mRNA	linear	EST 15-JUL-2002					
Db	780	GGGAATCTAGGCAATGAACCTAACAGATT--CTTTAAGAGCGTGATATTTTCATCAATGG	Bo691142	924 bp	mRNA	linear	EST 15-JUL-2002					
Qy	780	TCGCAGTTAGGAGAGATTAATTT 803	Bo691142	924 bp	mRNA	linear	EST 15-JUL-2002					
Db	840	GTGCGCATTTTAGGAGAGATTTT 863	Bo691142	924 bp	mRNA	linear	EST 15-JUL-2002					

FEATURES

Source

ORIGIN

Query Match	Best Local Similarity	43.6%	Score 750.2	DB 5	Length 924
Matches 781	Conservative	95.4%	Pred. No. 6.2e-196	Mismatches 37	Indels 1
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QY	92	GGCGCGCGCTGATCTCTGCTCTCTGGGCGCGCTGGGCTCCCTCTCCCTGGCGCCCTCC	151		
DB	164	GGCGCGCGCTGATCTCTCTCTGGGCGCGCTGGGCTCCCTCTCCCTGGCGCCCTCC	223		
QY	152	CCGACCTGGCGAAGACACAGAGAGTGGGACCTGGACCTTGACCTTCAACCCAGAGACCGCTGCA	211		
DB	224	CCGACCTGGCGAAGACACAGAGAGTGGGACCTGGACCTTGACCTTCAACCCAGAGACCGCTGCA	283		
QY	212	CTGCGTGAAGCCCTCGTCTCTGTCCTGTACCAATTAAGCGCAACCTGGCGACGACCGCG	271		
DB	284	CTGCGTGAAGCCCTCGTCTCTGTCCTGTACCAATTAAGCGCAACCTGGCGACGACCGCG	343		
QY	272	GTTCCCTCATCTCTGGGGTTCGCCAAGCTTCGTAACCTTGGCCAGAGGCTTGTCTCTGC	331		
DB	344	GTTCCCTCATCTCTGGGGTTCGCCAAGCTTCGTAACCTTGGCCAGAGGCTTGTCTCTGC	403		
QY	332	GTAACCTGAGTGTGGTGGCACCAAGACAGACTTCTTAATTTTCATCCCAAGAGAGATC	391		
DB	404	GTAACCTGAGTGTGGTGGCACCAAGACAGACTTCTTAATTTTCATCCCAAGAGAGATC	463		
QY	392	AACCTTTGAAGAGAGAAATTTACTGGCAATCTCAAGTCAACCAAGATATTTTGAATATG	451		
DB	464	AACCTTTGAAGAGAGAAATTTACTGGCAATCTCAAGTCAACCAAGATATTTTGAATATG	523		
QY	452	ATCCATCCCTCCTGATGTGAGAGAGAAATTAAGGTTGAGATGGCCCTACCAAGAGAAAT	511		
DB	524	ATCCATCCCTCCTGATGTGAGAGAGAAATTAAGGTTGAGATGGCCCTACCAAGAGAAAT	583		
QY	512	GCTACTCCGAGAAACATACCCAGAAAAATTTCAAGAACAGACCTTACTCAAGAGCTCTGT	571		
DB	584	GCTACTCCGAGAAACATACCCAGAAAAATTTCAAGAACAGACCTTACTCAAGAGCTCTGT	643		
QY	572	AGATGTGCTATACACTTTTGCAAACTGCTCAGAGACTGGAATGATGCTTTGGCCTAAATGC	631		
DB	644	AGATGTGCTATACACTTTTGCAAACTGCTCAGAGACTGGAATGATGCTTTGGCCTAAATGC	703		
QY	632	GTTATTAAGAACAGACAGATTTGCAAGTGGAAACAGTTTAAATGCTCAAGTCTCTCGAGCTA	691		
DB	704	GTTATTAAGAACAGACAGATTTGCAAGTGGAAACAGTTTAAATGCTCAAGTCTCTCGAGCTA	763		
QY	692	CTGCTCTTCAAGGGGATATTAACATTTCTTTGGGAAACTAGGCATATGAACCTTAACAGTTTCT	751		
DB	764	CTGCTCTTCAAGGGGATATTAACATTTCTTTGGGAAACTAGGCATATGAACCTTAAAGTTTCT	822		
QY	752	TAAAGAGCTGATATTTTCAATCAATGGGTGCGAGTTAGAGAGAAATTAATCAATGCA	811		
DB	823	TAAAGAGCTGATATTTTCAATCAATGGGTGCGAGTTAGAGAGAAATTAATCAATGCA	882		
QY	812	TAAACTTCAAGAAAGTCCACTTCAAAAATGCAAACT	850		
DB	883	TAAACTTCAAGAAAGTCCACTTCAAAAATGCAAACTCT	921		

RESULT	13
LOCUS	BQ438834
DEFINITION	BQ438834 907 bp mRNA EST 24-MAY-2007 AGENCOURT 7761619 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6017952
ACCESSION	BQ438834
VERSION	BQ438834.1 GI:21177910
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 (bases 1 to 907)
AUTHORS
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ULNL at:
<http://imgc.llnl.gov>
Plate: L14M13218 row: b column: 01
High quality sequence stop: 616.
Location/Qualifiers

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6017952"
/tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 70"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."

ORIGIN

Query Match 40.1%; Score 689.8; DB 5; Length 907;
Best Local Similarity 94.8%; Pred. No. 3.3e-179;
Matches 778; Conservative 0; Mismatches 34; Indels 9; Gaps 6;

385 AGAATCAACCTTTGAGAGAGAGATTACTGCAATCTCAAGTCAACGAGATATTTGCA 444
5 AAGAGTCAACCTTTGAGAGAGAGATTACTGCAATCTCAAGTCAACGAGATATTTGCA 64
445 AATATGATCCATCCCTCTGATGTGGAGAGAGATTACGTTGGATATGGCTTACCAAG 504
65 AATATGATCCATCCCTCTGATGTGGAGAGAGATTACGTTGGATATGGCTTACCAAG 124
505 AGCAATTCCTCTCGAGAACCTACCGAAGAAAGTTCAAGAACGACCTTAAGAA 564
125 AGCAATTCCTCTCGAGAACCTACCGAAGAAAGTTCAAGAACGACCTTAAGAA 184
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185 GCTCTGTAGATGTGCTATACATTTTGGAACTGCTCAGACTGGAATCTTTGGCC 244
625 TAAATGCTTATTAAGAACGACGATTTGGAGTGAACGATTATAGCTGCTGCTCC 684
245 TAAATGCTTATTAAGAACGACGATTTGGAGTGAACGATTATAGCTGCTGCTCC 304
685 TGGATCTAGCTCTCCAGGGGTATTAATTTCTTGGAACTAGCAATGAACCTAACA 744
305 TGGATCTAGCTCTCCAGGGGTATTAATTTCTTGGAACTAGCAATGAACCTAACA 364
745 GTTTCCTTAAGAGGCTGATATTTTCATCAATGAGTGCAGATTAGAGAGATTATATTC 804
365 GTTTCCTTAAGAGGCTGATATTTTCATCAATGAGTGCAGATTAGAGAGATTATATTC 424
805 AATTCATTAACCTTCTAAGAAAGTCCACTTAAATAATGCAAACTCTATGCTCTGATG 864
425 AATTCATTAACCTTCTAAGAAAGTCCACTTAAATAATGCAAACTCTATGCTCTGATG 484
865 TTGGTCAGGCTCGAAGAAAGCGGCTAAGATGCTGAAGGCTTCTGAAGGCTGGTGAAG 924
485 TTGGTCAGGCTCGAAGAAAGCGGCTAAGATGCTGAAGGCTTCTGAAGGCTGGTGAAG 544
925 AAGTATGATGATTCAGTTACATGATCACTAATATTTGATGAGCGGACTGCTACCA-G 982

Db 545 AAGTATGATGATTCAGTTACATGATCACTAATTTGAAAGGACGAGCTGACACGAG 604
Qy 983 GGAAGATTTTCTAACCCTGATGATTTGACATTTTATTCATCTG--TGCAAAAGTT 1040
Db 605 GGAAGATTTTCTAACCCTGATGATTTGACATTTTATTCATCTGTCGCAAAAGTTT 664
Qy 1041 TTCCAGGTGTTGAGACACGAGCCTGGCAAG-AAGTCTGTTAGAGAAACAGCTC 1099
Db 665 TTCCAGGTGTTGAGACACGAGCCTGGCAAGAGGCTGGTTAGAGAAACAGCTC 724
Qy 1100 TGCAATAT-GGAGGCGGAGCGCCCTTGTCTATCCGACACTTTGACAGCTGCTTATGTCG 1158
Db 725 TGCAATATGAGAGGAGGAGCGCCCTTGTCTATCCGACACTTTGACAGCTGCTTATGTCG 784
Qy 1159 T--GGATTAATTTGGGCTGTCTACGCCGGAATGGGAATGAA 1196
Db 785 TTGGATTAATTAATTTGGGCTGTCTACGCCGGAATGGGGAATGA 825

RESULT 14
B0775819/c 708 bp mRNA linear EST 26-JUL-2002
LOCUS
DEFINITION
UI-H-FH0-bcg-a-07-0-UI s1 NCI CGAP FH0 Homo sapiens CDNA clone
UI-H-FH0-bcg-a-07-0-UI 3', mRNA sequence.
ACCESSION
B0775819
VERSION
B0775819.1 GI:21984295
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 708)
AUTHORS
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Martin
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@iowa.edu
Seq primer: M13 FORWARD
POLY=A=yes.

FEATURES
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/tissue_type="Human Chondrosarcoma Cell line"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_1ib="NCI CGAP FH0"
/note="Organ: Bone; Vector: pRT3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I.
NCI CGAP FH0 is a CDNA library containing the following
tissue(s): Human Grade 1 Chondrosarcoma Cell line The
library was constructed according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. First strand
CDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pRT3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is AGAATCGGC. The cell line was provided by Dr
James Martin from University of Iowa
TAG TISSUE=Human Chondrosarcoma Cell line C58 - Grade 1
Chondrosarcoma


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Oy 1496 CCTTCTAAGACCTTTGGGACCTCATGATTACTTCCAAATCTGTCCAACTCAATGCT 1555
    |||
Db 487 CCTTCTAAGACCTTTGGGACCTCATGATTACTTCCAAATCTGTCCAACTCAATGCT 546
    |||
Oy 1556 AACTCTAAGAATGATGATGATCAAA-CCTGCGACCTTTAATGAAAAA-CCTCTCCG 1613
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Db 547 AACTCTAAGAATGATGATGATCAAAACCTTGCACCTTTAATGAAAAAACCCTCTCCG 606
    |||
Oy 1614 CCAGGAATTCACCTGGGCTTGCACGCTTTCATATAGTTTTTG 1659
    |||
Db 607 CCAGGAATTCACCTGGGCTTGCACGCTTTCATATAGTTTTTG 652
    |||
```

Search completed: March 2, 2005, 04:13:26
Job time : 5152 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 23:07:32 ; Search time 890 Seconds
(without alignments)
11447.050 Million cell updates/sec

Title: US-10-786-149-1
Perfect score: 1721
Sequence: 1 ctgagcttcctgactctccg.....atctactgctctgactctg 1721

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2859870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001s:*
5: geneseqn2002s:*
6: geneseqn2003s:*
7: geneseqn2004s:*
8: geneseqn2005s:*
9: geneseqn2006s:*
10: geneseqn2007s:*
11: geneseqn2008s:*
12: geneseqn2009s:*
13: geneseqn2010s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1721	100.0	1721	2	AAX35648
2	1721	100.0	1721	2	AAX35648
3	1721	100.0	1721	3	AAX39195
4	1721	100.0	1721	3	AAX75051
5	1721	100.0	1721	3	AAX33290
6	1721	100.0	1721	4	AAX91112
7	1721	100.0	1721	10	ADG88801
8	1721	100.0	1721	10	ADG88799
9	1721	100.0	1721	12	ADL16380
10	1721	100.0	1721	12	ADL16378
11	1721	100.0	1721	12	ADM48717
12	1719.4	99.9	1899	2	AA335650
13	1719.4	99.9	1899	3	AA335650
14	1719.4	99.9	1899	10	ADG88803
15	1719.4	99.9	1899	10	ADG88803
16	1719.4	99.9	1899	12	ADL16384
17	1719.4	99.9	1899	12	ADL16382
18	1719.4	99.9	1899	12	ADM48719
19	1719.4	99.9	1899	12	ADM48721
20	1713	99.5	1722	5	AAE93788

21	1694.6	98.5	1713	2	AAX37259	Aax37259 Human hep
22	1688.8	98.1	1723	2	AAX37260	Aax37260 Seq ID No
23	1686.8	98.0	3726	2	AAX86671	Aax86671 CDNA enco
24	1686.8	98.0	3726	10	ADD18951	Add18951 Human dis
25	1686.8	98.0	3726	12	ADK51968	Adk51968 Human ato
26	1686.8	98.0	3726	12	ADN04901	Adn04901 Antipori
27	1686.8	98.0	3726	13	ADN05073	Adn05073 Antipori
28	1686.8	98.0	3726	13	ADN080253	Adn080253 Hepatoma
29	1686.8	98.0	3726	14	ADP25078	Adp25078 PRO poly
30	1682.6	97.8	1724	4	AAH20940	Aah20940 Human hep
31	1648	95.8	1673	12	AD063816	Ad063816 Human hep
32	1648	95.8	1673	12	AD063817	Ad063817 Human hep
33	1646.4	95.7	1673	12	AD063818	Ad063818 Human hep
34	1631.4	94.8	1669	8	ABZ22816	Abz22816 Human hep
35	1631.4	94.8	1669	10	ADP16011	Adp16011 G-coupled
36	1629.8	94.7	1669	12	ADL93950	Adl93950 Human G-c
37	1585	92.1	1593	2	AA211236	Aa211236 Human pre
38	1554.2	90.3	1625	12	AD063819	Ad063819 ChimERIC
39	1554.2	90.3	1625	12	AD063820	Ad063820 ChimERIC
40	1552.6	90.2	1625	12	AD063821	Ad063821 ChimERIC
41	1535	89.2	1584	6	ABL40753	Ab140753 Chicken s
42	1535	89.2	1584	10	AA063532	Aa063532 ChimERIC
43	1092	63.5	2396	3	AA75081	Aa75081 CDNA enco
44	1092	63.5	2396	4	AA91113	Aa91113 Mouse hep
45	1092	63.5	2396	10	ADG88833	Adg88833 Mouse hpa

ALIGNMENTS

RESULT 1	
AAX35648	
ID AAX35648 standard; CDNA; 1721 BP.	
XX AAX35648;	
DT 09-JUL-1999 (first entry)	
XX	
DE CDNA encoding a human heparanase protein.	
XX	
KW Heparanase; hpa; modulator; heparin-binding growth factor;	
KW cellular response; cytokine; cell interaction; plasma lipoprotein;	
KW cellular susceptibility; infection; disintegration;	
KW neurodegenerative plaque; wound healing; angiogenesis; restenosis;	
KW atherosclerosis; inflammation; neurodegenerative disease; neuritis;	
KW plasma heparin; micrometastasis; autoimmune lesion; renal failure; BS.	
XX	
OS Homo sapiens.	
XX	
PN WO9911798-A1.	
XX	
PD 11-MAR-1999.	
XX	
PF 31-AUG-1998; 98WO-US017954.	
XX	
PR 02-SEP-1997; 97US-00922170.	
PR 02-JUL-1998; 98US-00109386.	
XX	
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.	
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.	
PA (FRIE/) FRIEDMAN M M.	
PI Pecker I, Vlodavsky I, Feinstein E,	
XX	
DR WPI; 1999-302255/25.	
DR P-PSDB; AAY02345.	
XX	
PT New human polynucleotide useful for treating angiogenesis, restenosis,	
PT and inflammation.	
XX	
PS Claim 4; Fig 1; 63p; English.	
XX	
CC The specification describes a polypeptide having heparanase (hpa)	

CC activity. The recombinant protein is used as a modulator of heparin-
 CC binding growth factors, cellular responses to heparin-binding growth
 CC factors and cytokines, cell interaction with plasma lipoproteins,
 CC cellular susceptibility to viral, protozoal and bacterial infections
 CC or disintegration of neurodegenerative plaques. Heparanase may be useful for
 CC conditions such as wound healing, angiogenesis, restenosis,
 CC atherosclerosis, inflammation, neurodegenerative diseases, and viral
 CC infections. Mammalian heparanase can be used to neutralize plasma
 CC heparin, and anti-heparanase antibodies may be applied for
 CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and
 CC renal failure in biopsy specimens, plasma samples, and body fluids. The
 CC present sequence encodes human heparanase

SO Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match 100.0%; Score 1721; DB 2; Length 1721;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CTGAGCTTTCGACTCCGCTGCGCGGCACTGCGGCGGAGAGACGAGGAGCCCA 60
Db 1 CTGAGCTTTCGACTCCGCTGCGCGGCACTGCGGCGGAGAGAGCCCA 60
QY 61 AGATGCTGCTGCGCTGGAAGCCCTGCGCTGCGCGGCTGATGCTGCTGCTGCGG 120
Db 61 AGATGCTGCTGCGCTGGAAGCCCTGCGCTGCGCGGCTGATGCTGCTGCTGCGG 120
QY 121 CGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 121 CGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 ACTGGAAGCTTTCACCGAGAGCCGCTGCACTGCTGAGAGCCCTGCTGCTGCTG 240
Db 181 ACTGGAAGCTTTCACCGAGAGCCGCTGCACTGCTGAGAGCCCTGCTGCTGCTG 240
QY 241 CCATGAGCGCAACCTGCGCAGGACCGCGGCTTCTCATCTCTGCGGCTTCTCAAG 300
Db 241 CCATGAGCGCAACCTGCGCAGGACCGCGGCTTCTCATCTCTGCGGCTTCTCAAG 300
QY 301 TTGCGTACCTTGGCGCAGAGGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 301 TTGCGTACCTTGGCGCAGAGGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 ACTTCCTAATTTTCGATCCCAAGAGATCACTTTGAAGAGAGATTAAGGCAAT 420
Db 361 ACTTCCTAATTTTCGATCCCAAGAGATCACTTTGAAGAGAGATTAAGGCAAT 420
QY 421 CTCAAGTCAACGAGATTTTGGCAATATGATCCCTCTGATGCTGAGAGAGAT 480
Db 421 CTCAAGTCAACGAGATTTTGGCAATATGATCCCTCTGATGCTGAGAGAGAT 480
QY 481 TACGTTTGAATGCGCTTACCGAGAGCAATGCTTACCTCCGAGAACATACCAAAA 540
Db 481 TACGTTTGAATGCGCTTACCGAGAGCAATGCTTACCTCCGAGAACATACCAAAA 540
QY 541 TCAGAGACAGCACTTCAAGAGCTCTGATGATGCTATACATTTTGGCAACGCT 600
Db 541 TCAGAGACAGCACTTCAAGAGCTCTGATGATGCTATACATTTTGGCAACGCT 600
QY 601 CAGAGCTGAGCTTATCTTGGCTTAATGCTTATTAAGAGAGAGATTTGCAATG 660
Db 601 CAGAGCTGAGCTTATCTTGGCTTAATGCTTATTAAGAGAGAGATTTGCAATG 660
QY 661 ACAATTGTAATGCTCACTGCTCTGAGCTTACCTCTTCAAGGGGATTAACATTT 720
Db 661 ACAATTGTAATGCTCACTGCTCTGAGCTTACCTCTTCAAGGGGATTAACATTT 720
QY 721 GGGAACTAGGAGATTAATCAATGTTCTTAAAGAGCTGATATTTTCAATGAG 780
Db 721 GGGAACTAGGAGATTAATCAATGTTCTTAAAGAGCTGATATTTTCAATGAG 780
QY 781 CGCAGTTAGAGAGATTAATCAATGATTAATCTTGAAGAGCTCACCCTTAA 840

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Db 781 CCAGTTAGAGAGATTAATCAATGATTAATCTTAAAGAGCTCACCCTTAA 840
QY 841 ATGCAAACTCATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 ATGCAAACTCATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
QY 901 AGAGCTTCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 AGAGCTTCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 TGAATGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Db 961 TGAATGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
QY 1021 TTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
Db 1021 TTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1081 GGTAGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1081 GGTAGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
QY 1141 CAGCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1141 CAGCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1201 TGATGAGAGAGAGATTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
Db 1201 TGATGAGAGAGAGATTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1261 CTTTACCTGATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db 1261 CTTTACCTGATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 TGGCAAGCTGCAAGGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 TGGCAAGCTGCAAGGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CTGCAATCAAGGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 CTGCAATCAAGGTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 TCACCAAGTACTTGGCTTACCTTCTTCTTCAAGAGAGAGAGAGAGAGAG 1500
Db 1441 TCACCAAGTACTTGGCTTACCTTCTTCTTCAAGAGAGAGAGAGAGAGAG 1500
QY 1501 TGAAGCTTGGAGCTTCAAGATTAATGCTTCAAGAGAGAGAGAGAGAGAG 1560
Db 1501 TGAAGCTTGGAGCTTCAAGATTAATGCTTCAAGAGAGAGAGAGAGAGAG 1560
QY 1561 TAAAGTGGTGGATGATCAAACTTGGCACTTAAATGAGAGAGAGAGAGAG 1620
Db 1561 TAAAGTGGTGGATGATCAAACTTGGCACTTAAATGAGAGAGAGAGAGAG 1620
QY 1621 GTTCACTGGGCTTGGCACTTCTCAATGATTTTGTGATGAAGAGAGAG 1680
Db 1621 GTTCACTGGGCTTGGCACTTCTCAATGATTTTGTGATGAAGAGAGAG 1680
QY 1681 CTGCTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1721
Db 1681 CTGCTTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1721

```

RESULT 2
 AAZ39195 standard; cDNA; 1721 BP.

AAZ39195;

02-MAR-2000 (first entry)

Human heparanase encoding cDNA.

QY 1261 CTTACCTGATATATGGCTATCTCTCTGTTCAAGAAATTGGTGGGCAACCAAGGTGTAA 1320
 DB 1261 CTTTACCTGATATATGGCTATCTCTCTGTTCAAGAAATTGGTGGGCAACCAAGGTGTAA 1320
 QY 1321 TGGCAAGCGTGCAAGGTTCAAGAGAAAGAGTTCAGATATACCTTCATTGGCAAAAC 1380
 DB 1321 TGGCAAGCGTGCAAGGTTCAAGAGAAAGAGTTCAGATATACCTTCATTGGCAAAAC 1380
 QY 1381 CTGCAATCCAGGTATTAAGAAAGAGATTTAACTCTGATGCGCATTAACCTTCATTAACG 1440
 DB 1381 CTGCAATCCAGGTATTAAGAAAGAGATTTAACTCTGATGCGCATTAACCTTCATTAACG 1440
 QY 1441 TCACCAAGTACTTGGCGTTACCTCATATCTTTTCTAACAAGCAAGTGAATTAATACCTTC 1500
 DB 1441 TCACCAAGTACTTGGCGTTACCTCATATCTTTTCTAACAAGCAAGTGAATTAATACCTTC 1500
 QY 1501 TAAGACCTTTGGGACCTTCATGATATTAATCTTCCAAATCTGTCCAACTCAATGGTCTAATC 1560
 DB 1501 TAAGACCTTTGGGACCTTCATGATATTAATCTTCCAAATCTGTCCAACTCAATGGTCTAATC 1560
 QY 1561 TAAAGATGTGTGATGATCAAAACCTTGCAACCTTTAATGAAAAAACCCTCCGCGCAGGAA 1620
 DB 1561 TAAAGATGTGTGATGATCAAAACCTTGCAACCTTTAATGAAAAAACCCTCCGCGCAGGAA 1620
 QY 1621 GTTCACTGGGCTTCCAGCTTTCTCATATATATATTTTTTTTGTGATTAAGAAATGCAAAAGTTG 1680
 DB 1621 GTTCACTGGGCTTCCAGCTTTCTCATATATATATTTTTTTTGTGATTAAGAAATGCAAAAGTTG 1680
 QY 1681 CTGCTTGACATCTGAAAAATTAATATCTATGCTGCTGACACTG 1721
 DB 1681 CTGCTTGACATCTGAAAAATTAATATCTATGCTGCTGACACTG 1721

RESULT 3
 AAA75051
 ID AAA75051 standard; cDNA; 1721 BP.
 AC AAA75051;
 XX
 DT 15-JAN-2001 (first entry)
 XX
 DE cDNA encoding a human heparanase polypeptide.
 XX
 KW Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
 KW heparin-binding growth factor; cytokine; neurodegenerative plaque;
 KW wound healing; infection; burn; angiogenesis; restenosis;
 KW atherosclerosis; inflammation; neurodegenerative disease;
 KW Gerstmann-Strausler Syndrome; Creutzfeldt-Jakob disease; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 63..1693
 FT /*tag= a
 FT /product= "heparanase"
 FT stem_loop 698..724
 FT /*tag= b
 FT /note= "these nucleotides are likely to be involved in
 FT forming stem and loop structures"
 XX
 FN W0200052178-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 14-FEB-2000; 2000MO-US003542.
 XX
 PR 01-MAR-1999; 99US-00258892.
 XX
 PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 PA (PRIE/) FRIEDMAN W M.

PI Pecker I, Vlodavsky I, Feinstein E;
 XX WPI; 2000-579289/54.
 DR P-PSDB; AAB08849.
 XX
 PT New polynucleotides encoding a polypeptide having heparanase activity,
 PT useful in wound healing and in gene therapy, particularly in treating
 PT tumor, inflammation, autoimmunity, neurodegenerative diseases.
 PS Claim 9; Fig 1; 152pp; English.
 XX
 CC The present sequence encodes a human protein with heparanase catalytic
 CC activity. The heparanase (hpa) polynucleotide is useful in gene therapy,
 CC particularly in treating tumour, inflammation or autoimmunity.
 CC Particularly, the polynucleotide is useful in modulating the
 CC bioavailability of heparin-binding growth factors, cellular responses to
 CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
 CC interleukin (IL)-8), cell interaction with plasma lipoproteins (e.g.
 CC susceptibility to certain viral and some bacterial and protozoa
 CC infections, or disintegration of neurodegenerative plaques. The
 CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
 CC radiation burns), and in the treatment of angiogenesis, restenosis,
 CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
 CC Strausler Syndrome or Creutzfeldt-Jakob disease), and some viral,
 CC bacterial or protozoa infections
 XX
 SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1721; DB 3; Length 1721;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAGAGCTTTGCACTCCGCTCGCGGCAAGCTGGGGGGAGACAGCCAGGTGAGCCCA 60
 DB 1 CTAGAGCTTTGCACTCCGCTCGCGGCAAGCTGGGGGGAGAGCCAGGTGAGCCCA 60
 QY 61 AGATGCTGCTGGGCTGGAAGCCCTGGGCTGCGCCCGCGCTGATGCTGCTCTGGGGC 120
 DB 61 AGATGCTGCTGGGCTGGAAGCCCTGGGCTGCGCCCGCGCTGATGCTGCTCTGGGGC 120
 QY 121 CGCTGGGTCCTCTCTGCTCCCTGGGCGCCCTGCGGACCTTGCAGACAGAGAGCTGTTG 180
 DB 121 CGCTGGGTCCTCTCTGCTCCCTGGGCGCCCTGCGGACCTTGCAGACAGAGAGCTGTTG 180
 QY 181 ACCTGACCTTCTTCAACCCAGAGCGCGCTGACCTGTGAGCCCTCTGCTCTGTCGCTCA 240
 DB 181 ACCTGACCTTCTTCAACCCAGAGCGCGCTGACCTGTGAGCCCTCTGCTCTGTCGCTCA 240
 QY 241 CCATTGACGCCCACTGGGCAAGGACCGCGGTTCTCTATCTCTGAGTTCTCCAAAGC 300
 DB 241 CCATTGACGCCCACTGGGCAAGGACCGCGGTTCTCTATCTCTGAGTTCTCTCAAGC 300
 QY 301 TTGTAACCTTGGCCAGAGGCTTGTCTCTGGTACCTGAGTTGGTGGCAAGACAG 360
 DB 301 TTGTAACCTTGGCCAGAGGCTTGTCTCTGGTACCTGAGTTGGTGGCAAGACAG 360
 QY 361 ACTTCTAATTTTCATCCCAAGAGAAATCACTTTGAAGAGAAAGTTAATGCGCAAT 420
 DB 361 ACTTCTAATTTTCATCCCAAGAGAAATCACTTTGAAGAGAAAGTTAATGCGCAAT 420
 QY 421 CTGAAGTCAACCAAGATATTTGCAAAATATGATCCATCCCTCTGATGTGAGAGAGAA 480
 DB 421 CTGAAGTCAACCAAGATATTTGCAAAATATGATCCATCCCTCTGATGTGAGAGAGAA 480
 QY 481 TACGGTTGGAAATGCGCCATACAGAGAGCAATGTCTACTCCGAAACACTACCAAAAAAGT 540
 DB 481 TACGGTTGGAAATGCGCCATACAGAGAGCAATGTCTACTCCGAAACACTACCAAAAAAGT 540
 QY 541 TCAAGAACAGCACTACTCAAGAGAGCTGTGATGATGCTATACACTTTTGAACAACTGCT 600
 DB 541 TCAAGAACAGCACTACTCAAGAGAGCTGTGATGATGCTATACACTTTTGAACAACTGCT 600
 QY 601 CAGAGCTGCACTTATCTTTGGCCTTAATGCGTTATTAAGAACAGAGATTTGCAAGTGA 660

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Db 601 CAGAGCTGGACTGATCTTTGGCCTAAATGCGTATATTAAGAACACAGATTGCACTGGA 660
Qy 661 ACAGTTCTAAAGCTCAGATGCTCCCTGGACTACTGCTCTTCCAGAGGGATTAACATTTCTT 720
Db 661 ACAGTTCTAAAGCTCAGATGCTCCCTGGACTACTGCTCTTCCAGAGGGATTAACATTTCTT 720
Qy 721 GGGAACTAGGCAATGAACTTAACAGTTTCCTTAAGAAAGGCTGATATTTTCATCAATGGAT 780
Db 721 GGGAACTAGGCAATGAACTTAACAGTTTCCTTAAGAAAGGCTGATATTTTCATCAATGGAT 780
Qy 781 CGCAGTTAGAGAGATTAATATTCATTAATGATTAACCTTCTAAGAAAGTCCACCTTCAAAA 840
Db 781 CGCAGTTAGAGAGATTAATATTCATTAATGATTAACCTTCTAAGAAAGTCCACCTTCAAAA 840
Qy 841 ATGCAAACTCTATAGTCTCTGATGTTGGTCAAGCTCCGAAAGAAAGACGGCTAAGATGCTGA 900
Db 841 ATGCAAACTCTATAGTCTCTGATGTTGGTCAAGCTCCGAAAGAAAGACGGCTAAGATGCTGA 900
Qy 901 AGAGCTTCTGAAAGGCTGGTGGAGAAAGTGAATTGATTCAAGTTACATGGCATCACTACTAT 960
Db 901 AGAGCTTCTGAAAGGCTGGTGGAGAAAGTGAATTGATTCAAGTTACATGGCATCACTACTAT 960
Qy 961 TGAATGGAACGAGCTGCTACCAAGGAAAGATTTTCTAAACCTGATGATTTGAACATTTTGA 1020
Db 961 TGAATGGAACGAGCTGCTACCAAGGAAAGATTTTCTAAACCTGATGATTTGAACATTTTGA 1020
Qy 1021 TTTTCATCTGTGCAAAAAGTTTCCAGGTGCTGAAGACCAAGGCTCGGCAAGAAAGGCTCT 1080
Db 1021 TTTTCATCTGTGCAAAAAGTTTCCAGGTGCTGAAGACCAAGGCTCGGCAAGAAAGGCTCT 1080
Qy 1081 GATTAGAGAGAAACAAGCTCTGCAATATGAGAGCGAGCGCCCTTGCTATCCGACACTTTTG 1140
Db 1081 GATTAGAGAGAAACAAGCTCTGCAATATGAGAGCGAGCGCCCTTGCTATCCGACACTTTTG 1140
Qy 1141 CAGCTGCTTTATGTGCTGATTAATTTGGGCTGTCAAGCCCGAAATGGGAATGAAGTGG 1200
Db 1141 CAGCTGCTTTATGTGCTGATTAATTTGGGCTGTCAAGCCCGAAATGGGAATGAAGTGG 1200
Qy 1201 TGAATGAGCAAGATATCTTTTGAAGAGCAAACTACCATTTATGATGATGAATCACTTCATC 1260
Db 1201 TGAATGAGCAAGATATCTTTTGAAGAGCAAACTACCATTTATGATGATGAATCACTTCATC 1260
Qy 1261 CTTTACCTGATTAATTTGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGCAACAAAGTGTAA 1320
Db 1261 CTTTACCTGATTAATTTGGCTATCTCTTCTGTTCAAGAAATTTGGTGGGCAACAAAGTGTAA 1320
Qy 1321 TGGCAAGCGTGCAGAGTTCAAGAGAGAGAGCTTCAAGTATACCTTCATTTGACAAACA 1380
Db 1321 TGGCAAGCGTGCAGAGTTCAAGAGAGAGAGCTTCAAGTATACCTTCATTTGACAAACA 1380
Qy 1381 CTGACATCCCAAGATTAATAAGAGAGATTTAACTCTGTATGCCATTAACCTCCCAATACG 1440
Db 1381 CTGACATCCCAAGATTAATAAGAGAGATTTAACTCTGTATGCCATTAACCTCCCAATACG 1440
Qy 1441 TCACCAAGATTAATGCGGTTAACCTCTCTTTCTTAACAAGCAAGTGGATTAATACCTTC 1500
Db 1441 TCACCAAGATTAATGCGGTTAACCTCTCTTTCTTAACAAGCAAGTGGATTAATACCTTC 1500
Qy 1501 TAAAGCTTTGGGACCTCATGATTAATCTTCCAAATCTGTCCAACTCAATGCTTAACTC 1560
Db 1501 TAAAGCTTTGGGACCTCATGATTAATCTTCCAAATCTGTCCAACTCAATGCTTAACTC 1560
Qy 1561 TAAAGATGATGATATCAAACTTCCCACTTTAATGAAAGAAACCTCTCCGGCAGAGAA 1620
Db 1561 TAAAGATGATGATATCAAACTTCCCACTTTAATGAAAGAAACCTCTCCGGCAGAGAA 1620
Qy 1621 GTTCACTGGGCTTGGCAGCTTCTCATATATGTTTTTTTGTGATTAAGAAATGCAAGTTG 1680
Db 1621 GTTCACTGGGCTTGGCAGCTTCTCATATATGTTTTTTTGTGATTAAGAAATGCAAGTTG 1680
Qy 1681 CTGCTTGATCTGAAATTAATAATATAGTCTGACACTG 1721
Db 1681 CTGCTTGATCTGAAATTAATAATATAGTCTGACACTG 1721
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Db 1681 CTGCTTGATCTGAAATTAATAATATAGTCTGACACTG 1721
RESULT 4
AAZ33290
ID AAZ33290 standard; cDNA; 1721 BP.
XX
AC AAZ33290;
XX
DT 21-FEB-2000 (first entry)
XX
DE Human heparanase nucleotide sequence.
XX
KW Human; heparanase; hpa; diagnosis; therapy; tumour; cytostatic;
KW antidiabetic; immunomodulatory; anti-inflammatory; nephrotropic;
KW metastasis; adenocarcinoma; squamous cell carcinoma; teratocarcinoma;
KW mesothelioma; melanoma; lymphoma; leukemia; cancer; sepsis; diabetes;
KW inflammation; haemorrhagic nephritis; nephrotic syndrome;
KW autoimmune disease; anticancer; kidney disease; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 63..1694
FT FT /tag=a
FT FT /product="heparanase"
XX
PM W09957153-A1.
XX
PD 11-NOV-1999.
XX
PF 29-APR-1999; 99WO-US009255.
XX
PR 01-MAY-1998; 98US-00071739.
XX
PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.
XX
PI Pecker I, Vlodavsky I, Friedman Y, Perets T;
XX
DR WP1; 2000-052944/04.
DR P-PSDB; AAY52990.
XX
PT Heparanase-specific molecular probes useful for diagnosis and treatment,
PT e.g. of tumors, and for targeted drug delivery.
XX
PS Example; Page 82-84; 90pp; English.
XX
CC The present invention describes heparanase-specific molecular probes,
CC useful for methods of detecting heparanase in situ. The probes and anti-
CC heparanase antibodies are used to detect or quantify the expression of
CC heparanase, for diagnosis and monitoring of diseases (especially
CC metastasis), for treatment of heparanase-associated diseases (e.g.
CC tumours, (adeno)carcinoma, squamous cell carcinoma, teratocarcinoma,
CC mesothelioma, melanoma, lymphoma or leukemia, a solid cancer (or its
CC metastases) derived from liver, prostate, bladder, breast, ovary, cervix,
CC colon, skin, intestine, stomach, uterus and pancreas, kidney disease,
CC diabetes and inflammation, haemorrhagic nephritis, nephrotic syndrome,
CC sepsis and inflammatory or autoimmune disease), for targeted drug
CC delivery (e.g. of anticancer agents) and as research reagents. The
CC present sequence encodes human heparanase, which is used in the
CC exemplification of the present invention
XX
SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;
Query Match 100.0%; Score 1721; DB 3; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CTAAGCTTTGCACTCTCCGCTGCGCGGCAAGCTGGCGGGGAGACAGCAGCTGAACCCA 60
Db 1 CTAAGCTTTGCACTCTCCGCTGCGCGGCAAGCTGGCGGGGAGACAGCAGCTGAACCCA 60
```

[illegible]

QY	1141	CAGTGGCTTATGTGGCTGGAATAATTGGGCTGTCAAGCCGAATGGAAATGAAAGTGG	1200
Db	1141	CAGTGGCTTATGTGGCTGGAATAATTGGGCTGTCAAGCCGAATGGAAATGAAAGTGG	1200
QY	1201	TGATGAGGCAAGATCTTTTGGAGCAGGAACTTACATTATGTGATGAAACTTCGATC	1260
Db	1201	TGATGAGGCAAGATCTTTTGGAGCAGGAACTTACATTATGTGATGAAACTTCGATC	1260
QY	1261	CTTTACCTGATTAATTGGCTATCTCTTGTCAAGAATGTGTGGGACCAAGGTGTAA	1320
Db	1261	CTTTACCTGATTAATTGGCTATCTCTTGTCAAGAATGTGTGGGACCAAGGTGTAA	1320
QY	1321	TGGCAAGCGTCGAAGGTTCAAGAGAGGAAGCTTCGATATACCTTCATTGCAACA	1380
Db	1321	TGGCAAGCGTCGAAGGTTCAAGAGAGGAAGCTTCGATATACCTTCATTGCAACA	1380
QY	1381	CTGACAAATCAAGATATTAAGAAGAGATTAACTCTGTATGCTATTAACCTTCATACG	1440
Db	1381	CTGACAAATCAAGATATTAAGAAGAGATTAACTCTGTATGCTATTAACCTTCATACG	1440
QY	1441	TGACCAAGTACTGGGATTACCTATCTTTTCTAACAGCAAGTGAATTAATACCTTC	1500
Db	1441	TGACCAAGTACTGGGATTACCTATCTTTTCTAACAGCAAGTGAATTAATACCTTC	1500
QY	1501	TAAAGCCTTTGGGACCTCATGSAATTAATCTTCGAAATGTGCCAATGTCTTAACTC	1560
Db	1501	TAAAGCCTTTGGGACCTCATGSAATTAATCTTCGAAATGTGCCAATGTCTTAACTC	1560
QY	1561	TAAAGATGTGATGATCAAACTTGGCACCTTTAATGGAATAAACCCTCCGGCAGGAA	1620
Db	1561	TAAAGATGTGATGATCAAACTTGGCACCTTTAATGGAATAAACCCTCCGGCAGGAA	1620
QY	1621	GTTACCTGGGCTTGCCGCTTTTCTCATATGTTTTTTTGTGATTAAGAAATGCCAAGTTG	1680
Db	1621	GTTACCTGGGCTTGCCGCTTTTCTCATATGTTTTTTTGTGATTAAGAAATGCCAAGTTG	1680
QY	1681	CTGCTTCATCTGAAATATAAATATATCTATGTCTTGACACTG 1721	
Db	1681	CTGCTTCATCTGAAATATAAATATATCTATGTCTTGACACTG 1721	

RESULT 5	
AAA91112	
ID	AAA91112 standard; DNA; 1721 BP.
XX	
AC	AAA91112;
XX	
DT	20-APR-2001 (first entry)
XX	
DE	Human heparanase, coding sequence fragment isolated from EST clone.
XX	
XX	Heparanase; hnp1; wound healing; angiogenesis; restenosis; Scurae;
XX	atherosclerosis; inflammation; pulmonary disease; Alzheimer's disease;
XX	neurodegenerative disease; Creutzfeldt-Jakob disease; viral infection;
XX	gene therapy; mouse; expressed sequence tag; db.
OS	Homo sapiens.
XX	
XX	W0200100643-A2.
PN	
XX	
PD	04-JAN-2001.
XX	
PF	19-JUN-2000; 2000WO-IL000358.
XX	
PR	25-JUN-1999; 99US-0140801P.
XX	
PA	(INSI-) INSIGHT STRATEGY & MARKETING LTD.
PI	
XX	Pecker I, Michal I, Itzhaki H;
DR	WPI; 2001-137930/14.
XX	
XX	New polynucleotides and polypeptides that are differentlv homologous to

PT heparanase, useful in wound healing, as well as in gene therapy protocols
PT for angiogenesis, restenosis, atherosclerosis, or inflammation.

XX Example 1; Page 67; 67pp; English.

XX This sequence represents a human heparanase coding sequence clone,
CC isolated from an EST clone. The invention relates to heparanase DNA and
CC protein sequences. The heparanase DNA and protein sequences are useful in
CC wound healing, angiogenesis, restenosis, atherosclerosis, inflammation,
CC pulmonary diseases, neurodegenerative diseases (such as Scurvy,
CC Alzheimer's disease, and Creutzfeldt-Jakob disease) or viral infections.
CC The heparanase coding sequence is particularly useful in gene therapy

SO Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match 100.0%; Score 1721; DB 4; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CTAGAGCTTTGAGCTCTCGCTGCGGCGAGCTGCGGGGAGAGCAGGCTGAGCCCA 60
DB 1 CTAGAGCTTTGAGCTCTCGCTGCGGCGAGCTGCGGGGAGAGCAGGCTGAGCCCA 60
QY 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCTGATGCTGCTCTGCGGAGC 120
DB 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGCTGATGCTGCTCTGCGGAGC 120
QY 121 CGCTGGGTCCTCTCTCCCTGCGCGCTGCGCGCGCTGCGCGAGCAGCAGCAGCAGC 180
DB 121 CGCTGGGTCCTCTCTCCCTGCGCGCTGCGCGCGCTGCGCGAGCAGCAGCAGCAGC 180
QY 181 AGCTGAGCTTCTTCAACCGAGAGCGCTGCACTGATGAGCGCGCTGCTCTGCTGCTCA 240
DB 181 AGCTGAGCTTCTTCAACCGAGAGCGCTGCACTGATGAGCGCGCTGCTCTGCTGCTCA 240
QY 241 CCATTGAGCGCAACCTGCGCAGGAGCCGCGGCTTCTCATCTCTCTGAGGTTCTCCAAAGC 300
DB 241 CCATTGAGCGCAACCTGCGCAGGAGCCGCGGCTTCTCATCTCTCTGAGGTTCTCCAAAGC 300
QY 301 TTCTGATCTTGGCCGAGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 TTCTGATCTTGGCCGAGAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 ACTTCTTAATTTTGGATCCCAAGAGAGATCAACTTTGAGAGAGAGATTAAGTGGCAAT 420
DB 361 ACTTCTTAATTTTGGATCCCAAGAGAGATCAACTTTGAGAGAGAGATTAAGTGGCAAT 420
QY 421 CTCAAGTCACAGAGATATTTGCAAAATATGATTCATCTCTGATGTGAGAGAGAGT 480
DB 421 CTCAAGTCACAGAGATATTTGCAAAATATGATTCATCTCTGATGTGAGAGAGAGT 480
QY 481 TACGGTTGGAATGCGCTTACCGAGAGCAATGCTCTCCGAGAGACCTACCGAGAGAGT 540
DB 481 TACGGTTGGAATGCGCTTACCGAGAGCAATGCTCTCCGAGAGACCTACCGAGAGAGT 540
QY 541 TCAAGAACAGACCTACTCAAGAGAGCTGTATGATGTGCTATACCTTTTGGAACTGCT 600
DB 541 TCAAGAACAGACCTACTCAAGAGAGCTGTATGATGTGCTATACCTTTTGGAACTGCT 600
QY 601 CAGGACTGGACTTGTATCTTTGGCTTAATGCTGATTAAGAACAGACAGATTTGACGTGA 660
DB 601 CAGGACTGGACTTGTATCTTTGGCTTAATGCTGATTAAGAACAGACAGATTTGACGTGA 660
QY 661 ACAGTTCTTAATGCTCAAGTTGCTCTGAGCTACTGCTCTTCCAAAGGAGTAAATTTCTT 720
DB 661 ACAGTTCTTAATGCTCAAGTTGCTCTGAGCTACTGCTCTTCCAAAGGAGTAAATTTCTT 720
QY 721 GGGAGCTAGGAGCAATAGCTTAACAGTTTCTTAAGAGGCTGATATTTTCAATGAGGT 780
DB 721 GGGAGCTAGGAGCAATAGCTTAACAGTTTCTTAAGAGGCTGATATTTTCAATGAGGT 780
QY 781 CGCAGTTAGAGAGATTAATATTCATATGCAATTAACCTTAAAGAGTCAACCTTCAAAA 840
DB 781 CGCAGTTAGAGAGATTAATATTCATATGCAATTAACCTTAAAGAGTCAACCTTCAAAA 840
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DB 781 CGCAGTTAGAGAGATTAATATTCATATGCAATTAACCTTAAAGAGTCAACCTTCAAAA 840
QY 841 ATGCAGAACTCTATAGTCTGATGTGCTGACCTCGAGAGAGAGCGGCTTAAGATGCTGA 900
DB 841 ATGCAGAACTCTATAGTCTGATGTGCTGACCTCGAGAGAGAGCGGCTTAAGATGCTGA 900
QY 901 AGACCTTCTGAGAGCTGCTGAGAGAGATGATGATTCAGTTACATGAGCATCACTAAT 960
DB 901 AGACCTTCTGAGAGCTGCTGAGAGAGATGATGATTCAGTTACATGAGCATCACTAAT 960
QY 961 TGAATGAGCGAGCTGCTACCGAGAGAAATTTTCTAAACCTCGATGATGACATTTTGA 1020
DB 961 TGAATGAGCGAGCTGCTACCGAGAGAAATTTTCTAAACCTCGATGATGATTTGACA 1020
QY 1021 TTTCATCTGTCGAGAGAGTTTTCAGAGGTGTTGAGAGACAGGCTGAGAGAGGCTCT 1080
DB 1021 TTTCATCTGTCGAGAGAGTTTTCAGAGGTGTTGAGAGACAGGCTGAGAGAGGCTCT 1080
QY 1081 GGTTAGAGAGAAACAGCTCTGCAATATGAGAGCGAGCGCTTGTCTATCCGACACCTTTG 1140
DB 1081 GGTTAGAGAGAAACAGCTCTGCAATATGAGAGCGAGCGCTTGTCTATCCGACACCTTTG 1140
QY 1141 CAGCTGCTTATATGCTGAGATTAATTTGGCTGTGACGCCGAGATGAGAAATAGAGTGG 1200
DB 1141 CAGCTGCTTATATGCTGAGATTAATTTGGCTGTGACGCCGAGATGAGAAATAGAGTGG 1200
QY 1201 TGATAGAGCAAGTATTTCTTGGAGCAGAGAACTACATTAAGTGAAGAACTTCGATC 1260
DB 1201 TGATAGAGCAAGTATTTCTTGGAGCAGAGAACTACATTAAGTGAAGAACTTCGATC 1260
QY 1261 CTTTACCTGATTAATTTGGCTATCTCTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTTAA 1320
DB 1261 CTTTACCTGATTAATTTGGCTATCTCTCTGTTCAAGAAATTTGGTGGGACCAAGGTGTTAA 1320
QY 1321 TGGCAAGCTGCAAGTTCAAGAGAGAAAGGCTTCCAGTATACCTTCATTTGCAACA 1380
DB 1321 TGGCAAGCTGCAAGTTCAAGAGAGAAAGGCTTCCAGTATACCTTCATTTGCAACA 1380
QY 1381 CTGACATCCAGAGTATTAAGAGAGAGATTAACCTGATAGCCATTAACCTCCATTAAG 1440
DB 1381 CTGACATCCAGAGTATTAAGAGAGAGATTAACCTGATAGCCATTAACCTCCATTAAG 1440
QY 1441 TCACCAAGTACTTCCGTTACCTTATCTTTTCTAAACAGAGTGAATTAACCTTC 1500
DB 1441 TCACCAAGTACTTCCGTTACCTTATCTTTTCTAAACAGAGTGAATTAACCTTC 1500
QY 1501 TAAAGCTTTGGAGCTCATGATGATTAATCTTCAAAATCTGTCAAACTCAATGCTTAACTC 1560
DB 1501 TAAAGCTTTGGAGCTCATGATGATTAATCTTCAAAATCTGTCAAACTCAATGCTTAACTC 1560
QY 1561 TAAAGATGAGTGAATGATCAAACTTGGCACTTTTAATGAGAAACCTCTCCGGCAGGAA 1620
DB 1561 TAAAGATGAGTGAATGATCAAACTTGGCACTTTTAATGAGAAACCTCTCTCCGGCAGGAA 1620
QY 1621 GTTCACTGGGCTTCCAGACTTCTCATATAGTTTGTGATTAAGAAATCCCAAGTTG 1680
DB 1621 GTTCACTGGGCTTCCAGACTTCTCATATAGTTTGTGATTAAGAAATCCCAAGTTG 1680
QY 1681 CTGCTTGATCTGAATAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAAT 1721
DB 1681 CTGCTTGATCTGAATAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAAT 1721
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RESULT 6
ADG88801
ID ADG88801 standard; cDNA; 1721 BP.
XX
AC ADG88801;
XX
XX 11-MAR-2004 (first entry)
DT
XX
DE Human hpa cDNA.
XX

KM Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
KM necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy;
KM gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
FT 63..1694
FT CDS /*tag= a
FT /product= "Human hpa protein"

US2003161823-A1.

XX 28-AUG-2003.

XX 14-JAN-2003; 2003US-00341582.

XX 31-AUG-1998; 98MO-US017954.

XX 01-MAR-1999; 98US-00258892.

XX 06-FEB-2001; 2001US-0076874.

XX 05-SEP-2001; 2001WO-IL000830.

XX 19-NOV-2001; 2001US-00988113.

XX (ILAN/) ILAN N.

XX (VLOD/) VLOD VSKY I.

XX (YACO/) YACOBY-ZEEVI O.

XX (PECK/) PECKER I.

XX (FEIN/) FEINSTEIN E.

XX ILAN N, Vlodavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;

XX WPI; 2003-897910/82.

XX P-PSDB; AD688800.

PT Composition for treating a wound comprising recombinant heparanase is
PT useful to induce or accelerate wound healing and induce or accelerate
PT angiogenesis.

XX Example 1; SEQ ID NO 11; 143pp; English.

CC The present invention relates to methods and compositions for inducing
CC and/or accelerating wound healing via the catalytic activity of
CC heparanase. The invention is used to induce or accelerate a healing
CC process, particularly of an ulcer, burn, laceration, surgical incision,
CC necrosis, pressure wound, diabetic ulcer and to induce or accelerate
CC angiogenesis. The present sequence is human hpa cDNA.

XX Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match 100.0%; Score 1721; DB 10; Length 1721; 1
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTAAGCTTTGACTCTCCGCTGCGCGAGCTGCGCGGAGAGACCCAGGTGAGCCCA 60
DB 1 CTAAGCTTTGACTCTCCGCTGCGCGAGCTGCGCGGAGAGACCCAGGTGAGCTCA 60
QY AGATGCTGCTGCGCTGCGAGCTGCGCTGCGCGCGCGCGCTGATGCTGCTCTCTGAGGC 120
DB AGATGCTGCTGCGCTGCGAGCTGCGCTGCGCGCGCGCGCTGATGCTGCTCTCTGAGGC 120
QY CGCTGCGTCCCTCTCTCCCTGCGCGCTGCGCGCGAGCTGCGCGAGCAAGAGAGTGTGG 180
DB CGCTGCGTCCCTCTCTCCCTGCGCGCTGCGCGCGAGCTGCGCGAGCAAGAGAGTGTGG 180
QY ACCGTGAGCTTCTTCAACCCAGAGAGCGGTGCACTGTGAGCCCTCGTTCCTGTCCGTCA 240
DB ACCGTGAGCTTCTTCAACCCAGAGAGCGGTGCACTGTGAGCCCTCGTTCCTGTCCGTCA 240
QY CCAATTGACGCAACCTGCGCGAGAGCGGTGCACTGTGAGCCCTCGTTCCTGTCCGTCA 300
DB CCAATTGACGCAACCTGCGCGAGAGCGGTGCACTGTGAGCCCTCGTTCCTGTCCGTCA 300

QY 301 TTGCACTTGGCCAGAGGCTTGTCTCTCGGTACTGAAGTTGTGTGACCAAGACAG 360
DB 301 TTGCACTTGGCCAGAGGCTTGTCTCTCGGTACTGAAGTTGTGTGACCAAGACAG 360
QY 361 ACTTCTTAATTTTGGATCCCAAGAGAGATCAACCTTGAAGAGAGATTAATGCGCAAT 420
DB 361 ACTTCTTAATTTTGGATCCCAAGAGAGATCAACCTTGAAGAGAGATTAATGCGCAAT 420
QY 421 CTCAAGTCAACCAAGATATTTGCAATATGATCATCCCTCGTATGATGAGAGAGAT 480
DB 421 CTCAAGTCAACCAAGATATTTGCAATATGATCATCCCTCGTATGATGAGAGAGAT 480
QY 481 TAGGTTGGAATGGCCCTTACCAAGAGCAATTTGTAATCCGAAACCTACCAAGAAAAGT 540
DB 481 TAGGTTGGAATGGCCCTTACCAAGAGCAATTTGTAATCCGAAACCTACCAAGAAAAGT 540
QY 541 TCAAGAACAGCACTTACTCAAGAGCTCTGTAGATGTCATACCTTTTGGCAACCTGCT 600
DB 541 TCAAGAACAGCACTTACTCAAGAGCTCTGTAGATGTCATACCTTTTGGCAACCTGCT 600
QY 601 CAGGACTGGAAGCTTATTTGCGCTTAATGCGTTATTAAGAACAGAGATTTGCACTGGA 660
DB 601 CAGGACTGGAAGCTTATTTGCGCTTAATGCGTTATTAAGAACAGAGATTTGCACTGGA 660
QY 661 ACAATTTCAATGCTCAAGTCTCTGAGCACTACCTCTTCCAGAGGATTAATCAATTTCTT 720
DB 661 ACAATTTCAATGCTCAAGTCTCTGAGCACTACCTCTTCCAGAGGATTAATCAATTTCTT 720
QY 721 GGGAACTGAGCAATGAACCTTAACAGTTTCTTAAGAGGCTGATATTTTCAATCAATGAGT 780
DB 721 GGGAACTGAGCAATGAACCTTAACAGTTTCTTAAGAGGCTGATATTTTCAATCAATGAGT 780
QY 781 CGCAGTTAGAGAGATTAATTAATTCATTCGATTAATCTTGAAGAAATCCACTTCAAAA 840
DB 781 CGCAGTTAGAGAGATTAATTAATTCATTCGATTAATCTTGAAGAAATCCACTTCAAAA 840
QY 841 ATGCAAACTCTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 900
DB 841 ATGCAAACTCTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 900
QY 901 AGAGCTTCTGAAAGCTGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 901 AGAGCTTCTGAAAGCTGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 961 TGAATGAGCGAGCTGCTCAAGAGAGATTTTCTAAACCTGATGATGATGATGATGATGAT 1020
DB 961 TGAATGAGCGAGCTGCTCAAGAGAGATTTTCTAAACCTGATGATGATGATGATGATGAT 1020
QY 1021 TTTCACTGTGCAAAAAGTTTCCAGTGCTGAGAGAGCAAGGCTGAGCAAGAGGCTCT 1080
DB 1021 TTTCACTGTGCAAAAAGTTTCCAGTGCTGAGAGAGCAAGGCTGAGCAAGAGGCTCT 1080
QY 1081 GGTGAGAGAGAAACAAGCTCTGATATGAGAGCGAGCGCTTGTGATCCGACACCTTTG 1140
DB 1081 GGTGAGAGAGAAACAAGCTCTGATATGAGAGCGAGCGCTTGTGATCCGACACCTTTG 1140
QY 1141 CAGCTGCTTATATGCTGATATATTTGGGCTGTGAGCCCGAATGAGATTAAGATGG 1200
DB 1141 CAGCTGCTTATATGCTGATATATTTGGGCTGTGAGCCCGAATGAGATTAAGATGG 1200
QY 1201 TGAATGAGCAAGATATTTTGAAGAGAGAACTTGAATGATGATGATGATGATGATGATG 1260
DB 1201 TGAATGAGCAAGATATTTTGAAGAGAGAACTTGAATGATGATGATGATGATGATGATG 1260
QY 1261 CTTTACCTGATATTTGAGCTATCTTCTGTTCAAGAAATTTGGGAGCAACCAAGGTGTAA 1320
DB 1261 CTTTACCTGATATTTGAGCTATCTTCTGTTCAAGAAATTTGGGAGCAACCAAGGTGTAA 1320
QY 1321 TGGCAAGGTCGCAAGGTTCAAGAGAGAGAGGCTTCAAGATATCTTCAATTTGCAACAA 1380
DB 1321 TGGCAAGGTCGCAAGGTTCAAGAGAGAGAGGCTTCAAGATATCTTCAATTTGCAACAA 1380
QY 1381 CTGACATTCAGATATTAAGAGAGAGATTTAACTGTATGCAATTAACCTTCATTAAG 1440

Db 1361 CTGACAAATCAAGATATAAAGAGAGATTAACTGTGATGCCATTAACCTCCATAACG 1440
Qy 1441 TCACCAATATCTGGGGTACCCCTATCCTTTTCTTAACAAGAAATGATTAATCCTTC 1500
Db 1441 TCACCAATATCTGGGGTACCCCTATCCTTTTCTTAACAAGAAATGATTAATCCTTC 1500
Qy 1501 TAAAGACTTGGGACCTCATGATGATTAATCTTCCAAATCTGTCCAACTCAATGGTCACTC 1560
Db 1501 TAAAGACTTGGGACCTCATGATGATTAATCTTCCAAATCTGTCCAACTCAATGGTCACTC 1560
Qy 1561 TAAAGATGTGGATGATCAAAACCTTGCCACCTTTAATGAAAAACCTCTCCGGCCAGAA 1620
Db 1561 TAAAGATGTGGATGATCAAAACCTTGCCACCTTTAATGAAAAACCTCTCCGGCCAGAA 1620
Qy 1621 GTTCACTGGGCTGGACCTTCTCATATAGTTTTTTTGTGATAGAAATGCAAAAGTTG 1680
Db 1621 GTTCACTGGGCTGGACCTTCTCATATAGTTTTTTTGTGATAGAAATGCAAAAGTTG 1680
Qy 1681 CTGCTTGATCTGAATAATTAATATATAGTCTGACACTG 1721
Db 1681 CTGCTTGATCTGAATAATTAATATATAGTCTGACACTG 1721

RESULT 7
ADG88799
ID ADG88799 standard; cDNA; 1721 BP.
XX
AC ADG88799;
XX
XX 11-MAR-2004 (first entry)
XX
DE Human hpa cDNA.
XX
KM Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
KW necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy;
KV gene; ss.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 63..1694
FT /tag= a
FT /product= "Human hpa protein"

XX
XX US2003161823-A1.
XX
XX 28-AUG-2003.
XX
XX 14-JAN-2003; 2003US-00341582.
XX
XX 31-AUG-1998; 98MO-US017954.
XX 01-MAR-1999; 99US-00258892.
XX 06-FEB-2001; 2001US-0076874.
XX 05-SEP-2001; 2001MO-IL000830.
XX 19-NOV-2001; 2001US-00988113.
XX
XX
XX (ILAN/) ILAN N.
XX (VLAD/) VLADAVSKY I.
XX (YACO/) YACOBY-ZEEVI O.
XX (PECK/) PECKER I.
XX (FEIN/) FEINSTEIN E.
XX
XX Ilan N, Vladavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;
XX
XX MPI, 2003-897910/82.
XX P-PSDB; ADG88800.
XX
XX Composition for treating a wound comprising recombinant heparanase is
XX PT useful to induce or accelerate wound healing and induce or accelerate
XX PT angiogenesis.
XX
XX Claim 4; SEQ ID NO 9; 143bp; English.

XX
CC The present invention relates to methods and compositions for inducing
CC and/or accelerating wound healing via the catalytic activity of
CC heparanase. The invention is used to induce or accelerate a healing
CC process, particularly of an ulcer, burn, laceration, surgical incision,
CC necrosis, pressure wound, diabetic ulcer and to induce or accelerate
CC angiogenesis. The present sequence is human hpa cDNA.
XX
SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match 100.0%; Score 1721; DB 10; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTAGAGCTTTGACCTCCGCTGCGCGGACCTGCGCGGGGGAGACAGCAGGTAGGCCA 60
Db 1 CTAGAGCTTTGACCTCCGCTGCGCGGACCTGCGCGGGGGAGACAGCAGGTAGGCCA 60
Qy 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGGCTGATGCTGCTGCGGGG 120
Db 61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCGCGCGGCTGATGCTGCTGCGGGG 120
Qy 121 CGCTGGGCTCCCTCTCCCTGCGCGCTGCGCGCGGCTGCGCGGCTGCGCGGCTG 180
Db 121 CGCTGGGCTCCCTCTCCCTGCGCGCTGCGCGCGGCTGCGCGGCTGCGCGGCTG 180
Qy 181 ACCTGAATCTTGAACCAAGAGCGGCTGCACTGCTGCTGCTGCTGCTGCTGCTG 240
Db 181 ACCTGAATCTTGAACCAAGAGCGGCTGCACTGCTGCTGCTGCTGCTGCTGCTG 240
Qy 241 CCATTGACGCCAAGCTGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 241 CCATTGACGCCAAGCTGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Qy 301 TTGCTACCTTGGCGAAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 301 TTGCTACCTTGGCGAAGGCTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Qy 361 ACTTCTTAATTTTGAATCCCAAGAGGAAATCACTTTGAAGAGAAATTAATGCGCA 420
Db 361 ACTTCTTAATTTTGAATCCCAAGAGGAAATCACTTTGAAGAGAAATTAATGCGCA 420
Qy 421 CTCAAGTCAACCAAGATATTTGCAATATGATTCATCCCTCTGATGTGAGAGAA 480
Db 421 CTCAAGTCAACCAAGATATTTGCAATATGATTCATCCCTCTGATGTGAGAGAA 480
Qy 481 TAGGTTGAATGAGCCCTTACAGAGCAATTTGCTTCCAGAACCTAACCAAAAAGT 540
Db 481 TAGGTTGAATGAGCCCTTACAGAGCAATTTGCTTCCAGAACCTAACCAAAAAGT 540
Qy 541 TCAAGAACAGACCTTACAGAGCAATTTGCTTCCAGAACCTAACCAAAAAGT 600
Db 541 TCAAGAACAGACCTTACAGAGCAATTTGCTTCCAGAACCTAACCAAAAAGT 600
Qy 601 CAGACTGCACTTATGCTTGGCTTAAATGCTTAAAGAGCTGATTTTCAATAGGCT 780
Db 601 CAGACTGCACTTATGCTTGGCTTAAATGCTTAAAGAGCTGATTTTCAATAGGCT 780
Qy 721 GGGAACTAGGAAAGAACTTAACGTTTCTTAAGAGGCTGATTTTCAATAGGCT 780
Db 721 GGGAACTAGGAAAGAACTTAACGTTTCTTAAGAGGCTGATTTTCAATAGGCT 780
Qy 781 CGCAGTTAGAGAGATTAATTAATGCAATTAATTTCAAGAGGCTCACTTCAAAA 840
Db 781 CGCAGTTAGAGAGATTAATTAATGCAATTAATTTCAAGAGGCTCACTTCAAAA 840
Qy 841 ATGCAAACTCTATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 ATGCAAACTCTATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900

QY 901 AGAGCTTCTGAAAGGCTGGGAGAGATGATGTTGATGTTACATGTCATCTACTATTT 960
DB 901 AGAGCTTCTGAAAGGCTGGGAGAGATGATGTTGATGTTACATGTCATCTACTATTT 960
QY 961 TGAATGAGACGACCTGCTACCAAGGAGATTTTCTTAAACCTGATGATGATGATTTTAA 1020
DB 961 TGAATGAGACGACCTGCTACCAAGGAGATTTTCTTAAACCTGATGATGATGATTTTAA 1020
QY 1021 TTTTCATCTGTCAAAAAGTTTTCAGAGGTGTTGAGACACAGGCTTGGCAAGAGTCT 1080
DB 1021 TTTTCATCTGTCAAAAAGTTTTCAGAGGTGTTGAGACACAGGCTTGGCAAGAGTCT 1080
QY 1081 GGTTCAGAGAAACAAGCTTGCATATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
DB 1081 GGTTCAGAGAAACAAGCTTGCATATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
QY 1141 CAGCTGGCTTTATGAGCTGATTAATTTGGGCTGTCAGCCGAAATGGGAAATGAGAGTGG 1200
DB 1141 CAGCTGGCTTTATGAGCTGATTAATTTGGGCTGTCAGCCGAAATGGGAAATGAGAGTGG 1200
QY 1201 TGATGAGGCAAGATATTTCTTGGAGCAAGAACTACCATTTAGTGAATGAAACTTCGATC 1260
DB 1201 TGATGAGGCAAGATATTTCTTGGAGCAAGAACTACCATTTAGTGAATGAAACTTCGATC 1260
QY 1261 CTTTACCTGATTAATTTGGCTATCTCTTCTGTTCAAGAAATTTGGTGGCACCAAGTGTAA 1320
DB 1261 CTTTACCTGATTAATTTGGCTATCTCTTCTGTTCAAGAAATTTGGTGGCACCAAGTGTAA 1320
QY 1321 TGGCAAGCGTCAAGGCTTCAAGAGAGAGAGAGGATTTGATTAATCTTCAATGTCACAAACA 1380
DB 1321 TGGCAAGCGTCAAGGCTTCAAGAGAGAGAGAGGATTTGATTAATCTTCAATGTCACAAACA 1380
QY 1381 CTGACATCTCAAGATTAATTAAGAGAGATTTAACTGTATGCTCAATTAACCTCCATTAACG 1440
DB 1381 CTGACATCTCAAGATTAATTAAGAGAGATTTAACTGTATGCTCAATTAACCTCCATTAACG 1440
QY 1441 TCACCAAGTACTTGGGCTTACCTTATCTTCTTCAAGAGAGATTTAACTGTATGCTCAATTAACG 1500
DB 1441 TCACCAAGTACTTGGGCTTACCTTATCTTCTTCAAGAGAGATTTAACTGTATGCTCAATTAACG 1500
QY 1501 TAAAGCTTTGGGACCTCATGATTAATCTTCAATCTGTCCAAATCTGATGATGATGATGATG 1560
DB 1501 TAAAGCTTTGGGACCTCATGATTAATCTTCAATCTGTCCAAATCTGATGATGATGATGATG 1560
QY 1561 TAAAGATGATGATGATCAAACTTGGCACTTTAAATGAGAAACCTCTCCGCGCAGAGAA 1620
DB 1561 TAAAGATGATGATGATCAAACTTGGCACTTTAAATGAGAAACCTCTCCGCGCAGAGAA 1620
QY 1621 GTTCACTGGGCTTGGCAGCTTTCATATAGTTTTTTTGTGATTAAGAAATGCAAAAGTTG 1680
DB 1621 GTTCACTGGGCTTGGCAGCTTTCATATAGTTTTTTTGTGATTAAGAAATGCAAAAGTTG 1680
QY 1681 CTGCTTGGATCTGAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1721
DB 1681 CTGCTTGGATCTGAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1721

RESULT 8
ADL16380
ID ADL16380 standard; cDNA; 1721 BP.

AC ADL16380;

XX 06-MAY-2004 (first entry)

DE Human heparanase partial cDNA #2.

XX Human; ss; heparanase; gene; heparanase-dependent cancer; cancer;

OS autoimmunity reaction; inflammation; chromosome 4.

XX Homo sapiens.

PN US2003236215-A1.
XX 25-DEC-2003.
PD
PP 09-JUN-2003; 2003US-00456573.
PR 31-AUG-1998; 98WO-US017954.
PR 01-MAR-1999; 99US-00258892.
PR 08-NOV-1999; 99US-00435739.
PA (INST-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASTI MEDICAL RES SERVICES & DEV.
PI Pecker I, Vlodavsky I, Feinstein E;
PI WPI; 2004-070610/07.
PT New antisense oligonucleotide hybridizable with a polynucleotide encoding
PT a polypeptide with heparanase activity, useful for treating diseases such
PT as cancer and autoimmune disorders.
PS Example 1; SEQ ID NO 11; 108bp; English.
XX The invention relates to an antisense oligonucleotide (ASO) comprising a
XX hybridizable in vivo, under physiological conditions, with a portion of
XX a polynucleotide strand encoding a polypeptide having heparanase
XX catalytic activity. Also included are a method of in vivo downregulating
XX heparanase activity (comprising administering the ASO in vivo), a method
XX of treating a subject suffering from a pathological condition
XX (characterised by heparanase activity, comprising administering ASO to
XX the subject), a pharmaceutical composition comprising the ASO and a
XX carrier, an antisense nucleic acid construct (comprising the ASO and a
XX sequence and a polynucleotide sequence directing the synthesis of an
XX antisense RNA sequence of at least 10 bases being hybridizable in vivo,
XX under physiological conditions, with a polynucleotide strand encoding a
XX polypeptide having heparanase catalytic activity), a method of in vivo
XX downregulating heparanase activity (comprising administering in vivo the
XX antisense nucleic acid construct), a pharmaceutical composition
XX comprising the antisense nucleic acid construct and a carrier, and an
XX analogue of at least 10 bases being hybridizable in vivo, under
XX physiological conditions, with a portion of a polynucleotide strand being
XX characterised by forming at least a portion of an untranslated region
XX (UTR) for a polynucleotide strand encoding a polypeptide having
XX heparanase catalytic activity. The methods and compositions of the
XX present invention are useful for the prevention and/or treatment of
XX diseases or conditions associated with aberrant heparanase activity, such
XX as heparanase-dependent cancer, cancer, autoimmune reaction and
XX inflammation. The gene for human heparanase is located on chromosome 4.
XX The present sequence is a human heparanase cDNA.
SQ Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;
Query Match 100.0%; Score 1721; DB 12; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTAGAGCTTTCGACTCCGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
DB 1 CTAGAGCTTTCGACTCCGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 60
QY 61 AGATGCTGTGCGCTGGAAGCTGCGCTGCGCGCGCTGATGCTGCTGCTGCGGCGC 120
DB 61 AGATGCTGTGCGCTGGAAGCTGCGCTGCGCGCGCTGATGCTGCTGCTGCGGCGC 120
QY 121 CGCTGGGTCCCTCTCCCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGC 180
DB 121 CGCTGGGTCCCTCTCCCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGCTGCGGCGC 180
QY 181 ACCTGGAATTTTACCAAGAGCGCTGCACTGATGAGCCCTGCTGCTGCTGCTGCTGCA 240
DB 181 ACCTGGAATTTTACCAAGAGCGCTGCACTGATGAGCCCTGCTGCTGCTGCTGCTGCA 240

polynucleotide or a polynucleotide analogue of at least 10 bases being hybridisable *in vivo*, under physiological conditions, with a portion of a polynucleotide strand encoding a polypeptide having heparanase catalytic activity. Also included are a method of *in vivo* downregulating heparanase activity (comprising administering the ASO *in vivo*), a method of treating a subject suffering from a pathological condition (characterised by heparanase activity, comprising administering ASO to the subject), a pharmaceutical composition comprising administering ASO to a carrier, an antisense nucleic acid construct (comprising the ASO and a sequence and a polynucleotide sequence directing the synthesis of an antisense RNA sequence of at least 10 bases being hybridisable *in vivo*, under physiological conditions, with a polynucleotide strand encoding a polypeptide having heparanase catalytic activity), a method of *in vivo* downregulating heparanase activity (comprising administering *in vivo* the antisense nucleic acid construct), a pharmaceutical composition comprising the antisense nucleic acid construct and a carrier, and an antisense oligonucleotide comprising a polynucleotide or a polynucleotide analogue of at least 10 bases being hybridisable *in vivo*, under physiological conditions, with a portion of a polynucleotide strand being characterised by forming, at least a portion of an untranslated region (UTR) for a polynucleotide strand encoding a polypeptide having heparanase catalytic activity. The methods and compositions of the present invention are useful for the prevention and/or treatment of diseases or conditions associated with aberrant heparanase activity, such as heparanase-dependent cancer, cancer, autoimmune reaction and inflammation. The gene for human heparanase is located on chromosome 4. The present sequence is a human heparanase cDNA.

Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1721;	DB 12;	Length 1721;
Best Local Similarity	100.0%;	Prod n=0		

Accuracy	100.00%	Pred. No. 0
Matches	1721	Conservative 0
		Mismatches

Model	0	Gaps	0
0	0	0	0

QY 1 CTAAGCTTTCGACTCTCCGCTGCGGCGAGCTGGCGGGGGAGAGCAAGCCAGGTGAGCCCA 60
 Db 1 CTAAGCTTTCGACTCTCCGCTGCGGCGAGCTGGCGGGGGAGAGCAAGCCAGGTGAGCCCA 60
 QY 61 AGATGCTGCTGCGCGCTGGAGGCTTGGCCCTGCGCGCGCGCTGATGCTGCTCTCGAGGC 120
 Db 61 AGATGCTGCTGCGCGCTGGAGGCTTGGCCCTGCGCGCGCGCTGATGCTGCTCTCGAGGC 120
 QY 121 CGCTGGAGTCCCTCTCTCCCTGGCGGCTCTCCCGACCTGGCGGAGACAGAGAGCTCGTG 180
 Db 121 CGCTGGAGTCCCTCTCTCCCTGGCGGCTCTCCCGACCTGGCGGAGACAGAGAGCTCGTG 180
 QY 181 ACCTGGACCTTCTTACCCAGAGAGCGGCTGCACTGTGTAGGCCCTCGTCTCTGTCGGTCA 240
 Db 181 ACCTGGACCTTCTTACCCAGAGAGCGGCTGCACTGTGTAGGCCCTCGTCTCTGTCGGTCA 240
 QY 241 CCAATTGACGCAACCTGGCGCACGAGACCGGCGGTTCTTCATCTCTCTGGGTTTTCGAAAGC 300
 Db 241 CCAATTGACGCAACCTGGCGCACGAGACCGGCGGTTCTTCATCTCTCTGGGTTTTCGAAAGC 300
 QY 301 TTGGTACCTTGGCCAGAGGCTTGTCTCTGCGGTACTGAGGTTGGTGAGCAACAAGC 360
 Db 301 TTGGTACCTTGGCCAGAGGCTTGTCTCTGCGGTACTGAGGTTGGTGAGCAACAAGC 360
 QY 361 ACTTCTAATTTTGCATCCCAAGAGAAATCAACTTTGAAAGAGAGTTACTGGCAAT 420
 Db 361 ACTTCTAATTTTGCATCCCAAGAGAAATCAACTTTGAAAGAGAGTTACTGGCAAT 420
 QY 421 CTCAAGTCAACAGAGATTTTGCATAATATGATTCATCCCTCGTATGTGGAGGAAAGT 480
 Db 421 CTCAAGTCAACAGAGATTTTGCATAATATGATTCATCCCTCGTATGTGGAGGAAAGT 480
 QY 481 TACGTTGGATGGCCCTTACAGAGAGCAATTGCTATCTCGAGAACTACCAAGAAAAAGT 540
 Db 481 TACGTTGGATGGCCCTTACAGAGAGCAATTGCTATCTCGAGAACTACCAAGAAAAAGT 540
 QY 541 TCAAGAACAGACACTTACTCAAGAGCTGTGATGTGCTATATACCTTTTGGAACTGCT 600
 Db 541 TCAAGAACAGACACTTACTCAAGAGCTGTGATGTGCTATATACCTTTTGGAACTGCT 600

QY	601	CAGACCTGACCTTGATCTTTGGCCTTAAATGCGTTATTAAAGACAGCATTTTGCAGTGA	660
Db	601	CAGACCTGACCTTGATCTTTGGCCTTAAATGCGTTATTAAAGACAGCATTTTGCAGTGA	660
QY	661	ACAGTCTTAATGCTCAGTTGGCTCTCGGACCTACCTGCTTCCAGGGGTATTAACATTTCTT	720
Db	661	ACAGTCTTAATGCTCAGTTGGCTCTCGGACCTACCTGCTTCCAGGGGTATTAACATTTCTT	720
QY	721	GGGACCTAAGCAATGACCTTAACAGTTTCTTAAAGAGCGTATTTTCAATCAATGGGT	780
Db	721	GGGACCTAAGCAATGACCTTAACAGTTTCTTAAAGAGCGTATTTTCAATCAATGGGT	780
QY	781	CCGAGTTTGGAGGAAGATTATTTCAATTGCATTAACCTTCTAAGAAATGCACTTCAAA	840
Db	781	CCGAGTTTGGAGGAAGATTATTTCAATTGCATTAACCTTCTAAGAAATGCACTTCAAA	840
QY	841	ATGCAAAACTCTATGTCCTGATGTTTGGTCAGCGCTGAAAGAAAGCGCTAAGTGTGA	900
Db	841	ATGCAAAACTCTATGTCCTGATGTTTGGTCAGCGCTGAAAGAAAGCGCTAAGTGTGA	900
QY	901	AGAGCTTCCGTAAGGCTGTGTGAGAAATGATTTCACTTACATGCGATCACTACTAT	960
Db	901	AGAGCTTCCGTAAGGCTGTGTGAGAAATGATTTCACTTACATGCGATCACTACTAT	960
QY	961	TGAATGACGGAATGCTCAACAGGAGATTTTCTTAAACCTGTATGTAATTTGACATTTT	1020
Db	961	TGAATGACGGAATGCTCAACAGGAGATTTTCTTAAACCTGTATGTAATTTGACATTTT	1020
QY	1021	TTTTCATCTGTGCAAAAAGTTTTCAGTGGTTGAGAGCACAGGCTGTGCAAGAAAGTCT	1080
Db	1021	TTTTCATCTGTGCAAAAAGTTTTCAGTGGTTGAGAGCACAGGCTGTGCAAGAAAGTCT	1080
QY	1081	GATTAGAGAAACAAGCTCTGCAATTTGAGAGCGGAGCGCCTTGTCTATCCGACACCTT	1140
Db	1081	GATTAGAGAAACAAGCTCTGCAATTTGAGAGCGGAGCGCCTTGTCTATCCGACACCTT	1140
QY	1141	CAGCTGGCTTTATGTGCTGATTAATTTGGCCTGTCAAGCCGAAATGGAGATTTGAAATGG	1200
Db	1141	CAGCTGGCTTTATGTGCTGATTAATTTGGCCTGTCAAGCCGAAATGGAGATTTGAAATGG	1200
QY	1201	TGATGAGCAATATTTCTTTGAGAGAGGAAACTTCAATTTATGTGATGAAACCTTGATC	1260
Db	1201	TGATGAGCAATATTTCTTTGAGAGAGGAAACTTCAATTTATGTGATGAAACCTTGATC	1260
QY	1261	CTTTACCTGATTTATTTGGCTATCTCTTCTGTTCAGAAATTTGGTGGCACCMAGATTTA	1320
Db	1261	CTTTACCTGATTTATTTGGCTATCTCTTCTGTTCAGAAATTTGGTGGCACCMAGATTTA	1320
QY	1321	TGCAAGAGGTGCAAGGTTCAAAAGAGAAAGCTTGAATATCTTCAATTTGCACAAACA	1380
Db	1321	TGCAAGAGGTGCAAGGTTCAAAAGAGAAAGCTTGAATATCTTCAATTTGCACAAACA	1380
QY	1381	CTGACATCCAAAGGTATTAAGAGAGATTTAACTGTATGCGATTAACCTGCCATAAG	1440
Db	1381	CTGACATCCAAAGGTATTAAGAGAGATTTAACTGTATGCGATTAACCTGCCATAAG	1440
QY	1441	TCACAAGTCTTGGCGTTACCTTATCCCTTTTCTTAAACAAGACGTGATTAATCTTTC	1500
Db	1441	TCACAAGTCTTGGCGTTACCTTATCCCTTTTCTTAAACAAGACGTGATTAATCTTTC	1500
QY	1501	TAAAGCTTTGGGACCTCAATGATTAACCTTCCAAATCTGTCCAACTCAATGATGTTAACTC	1560
Db	1501	TAAAGCTTTGGGACCTCAATGATTAACCTTCCAAATCTGTCCAACTCAATGATGTTAACTC	1560
QY	1561	TAAAGATGATGATTAACCTTTCGACCTTTTATGGAATACTCTCGGCGAAGAA	1620
Db	1561	TAAAGATGATGATTAACCTTTCGACCTTTTATGGAATACTCTCGGCGAAGAA	1620
QY	1621	GTTCACTGAGGCTTGCAGCTTTCTCATATAGTTTTTTGTGATGAAGAAATGCCAAAGTTG	1680
Db	1621	GTTCACTGAGGCTTGCAGCTTTCTCATATAGTTTTTTGTGATGAAGAAATGCCAAAGTTG	1680


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Db      1021 TTTCATCTGTGCAAAAAAGTTTTCAGGTGGTGGAGAGACAGAGCGCTGGCAAGAGCTCT 1080
Qy      1081 GGTTAGAGAAAACAAGCTCTGATATGAGAGGGAGCGCCCTTGTATCCAGACCTTTG 1140
Db      1081 GGTTAGAGAAAACAAGCTCTGATATGAGAGGGAGCGCCCTTGTATCCAGACCTTTG 1140
Qy      1141 CAGCTGGCTTTATGAGCTGTGATTAATGGGCTGTGAGCCCGAATGGGAATAGAACTGG 1200
Db      1141 CAGCTGGCTTTATGAGCTGTGATTAATGGGCTGTGAGCCCGAATGGGAATAGAACTGG 1200
Qy      1201 TGATGAGGCAAGTATCTTTGGAGAGAAAATACCACTTATGATGAGAAAACCTTGGATC 1260
Db      1201 TGATGAGGCAAGTATCTTTGGAGAGAAAATACCACTTATGATGAGAAAACCTTGGATC 1260
Qy      1261 CTTTACCTGATTTATGCTATCTCTTCTGTCAAGAAATGGTGGGACCAAGGTGTTA 1320
Db      1261 CTTTACCTGATTTATGCTATCTCTTCTGTCAAGAAATGGTGGGACCAAGGTGTTA 1320
Qy      1321 TGGCAAGCGTCAAGGTTCAAGAGAGAGAAAGCTTGGATTAACCTTCAATTGCAAAACA 1380
Db      1321 TGGCAAGCGTCAAGGTTCAAGAGAGAGAAAGCTTGGATTAACCTTCAATTGCAAAACA 1380
Qy      1381 CTGACATCCCAAGGTATTAAGAGAGAGATTTAACTGTATGCGATTAACCTTCAATAG 1440
Db      1381 CTGACATCCCAAGGTATTAAGAGAGAGATTTAACTGTATGCGATTAACCTTCAATAG 1440
Qy      1441 TCACCAAGTACTTGGCGGTACCTATCTCTTCTTCAACAAGCAAGTGATTAATACCTTC 1500
Db      1441 TCACCAAGTACTTGGCGGTACCTATCTCTTCTTCAACAAGCAAGTGATTAATACCTTC 1500
Qy      1501 TAAGACCTTTGGGACCTCATGATTACTTCCAAATCTGTCCAACTCAATGGTCTTAAC 1560
Db      1501 TAAGACCTTTGGGACCTCATGATTACTTCCAAATCTGTCCAACTCAATGGTCTTAAC 1560
Qy      1561 TAAAGATGGTGAATGATTAACAACCTTCCCACTTTAAATGGAACCTCTCGGCGCAGAA 1620
Db      1561 TAAAGATGGTGAATGATTAACAACCTTCCCACTTTAAATGGAACCTCTCGGCGCAGAA 1620
Qy      1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAGAAATGCCAAAGTTG 1680
Db      1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAGAAATGCCAAAGTTG 1680
Qy      1681 CTGCTGGCATCTGAATAATTAATATATCTAGTCTGACACTG 1721
Db      1681 CTGCTGGCATCTGAATAATTAATATATCTAGTCTGACACTG 1721

RESULT 11
ADM48715
ID      ADM48715 standard; cDNA, 1721 BP.
AC      ADM48715;
DT      03-JUN-2004 (first entry)
XX      Human hpa cDNA.
XX      Transgenic animal; heparinase; cancer; viral infection; reestenosis;
XX      neurodegenerative disease; atherosclerosis; pulmonary disorder; hpa;
XX      human; gene; ss.
OS      Homo sapiens.
XX      Key      Location/Qualifiers
XX      FT      CDS      63..1694
XX      FT      /tag= a
XX      FT      /product= "Hpa protein"
XX      PN      US2003217375-A1.
XX      PD      20-NOV-2003.
XX      PF      24-FEB-2003; 2003US-00371218.

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XX      31-AUG-1998; 98WO-US017954.
PR      01-MAR-1999; 99US-0025892.
PR      06-FEB-2001; 2001US-00776874.
PR      19-NOV-2001; 2001US-00988113.
XX      (ZCHA/) ZCHARIA E.
PA      (VL0D/) VL0DAVSKY I.
PA      (METZ/) METZGER S.
PA      (BECK/) PECKER I.
PA      (ILAN/) ILAN N.
PA      (CHAJ/) CHAJEK-SHAUL T.
PA      (GOLD/) GOLDSHMIDT O.
XX      Zcharia E, Vlodayevsky I, Metzger S, Pecker I, Ilan N,
PI      Chajek-Shaul T, Goldshmidt O,
DR      WPI; 2004-021916/02.
DR      P-PsDB; ADM48716.
XX      New transgenic non-human animal expressing heparinase, useful as models
PT      for human disease, such as cancers, viral infection, neurodegenerative
PT      diseases, reestenosis, atherosclerosis and pulmonary disorders.
XX      Example 1; SEQ ID NO 9; 106bp; English.
XX      The present invention relates to a transgenic non-human animal whose
CC      genome comprises an exogenous polynucleotide sequence, including a
CC      promoter active in tissues of the non-human, a region encoding a human
CC      heparinase, where the promoter and the region encoding human heparinase
CC      are operably linked in the exogenous polynucleotide such that human
CC      heparinase is expressed in at least a portion of the cells of the non-
CC      human animal. The methods and compositions of the present invention are
CC      useful for the production of transgenic animals expressing heparinase, to
CC      be used as models for human diseases such as cancers, viral infection,
CC      reestenosis, neurodegenerative diseases, atherosclerosis and pulmonary
CC      disorders. The present sequence is human hpa cDNA used in the
CC      exemplification of the invention.
SQ      Sequence 1721 BP; 451 A; 413 C; 410 G; 447 T; 0 U; 0 Other;
Query Match      100.0%; Score 1721; DB 12; Length 1721;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1721; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 CTAGAGCTTTGAGACTCCCGCTGCGCGGCAAGCTGGCGGGGAGAGCAGGTGAGCCCA 60
Db      1 CTAGAGCTTTGAGACTCTCCGCTGCGCGGCAAGCTGGCGGGGAGAGCAGGTGAGCCCA 60
Qy      61 AGATGCTGCTGCGCTGCAAGGCTGCGTGGCGCGCGCGGCTGATGCTGCTGCTGGGCG 120
Db      61 AGATGCTGCTGCGCTGCAAGGCTGCGTGGCGCGCGCGGCTGATGCTGCTGCTGGGCG 120
Qy      121 CGCTGGGTCCTCCCTGCGCGCGCTGCGCGGCTGCGGACCTGGCGAGCAGAGAGTCTGG 180
Db      121 CGCTGGGTCCTCCCTGCGCGCGCTGCGCGGCTGCGGACCTGGCGAGCAGAGAGTCTGG 180
Qy      181 ACCTGACCTTCTCACCAGCAGAGCGCTGACCTGTGAGGCCCTGCTCTGCTGCTCA 240
Db      181 ACCTGACCTTCTCACCAGCAGAGCGCTGACCTGTGAGGCCCTGCTCTGCTGCTCA 240
Qy      241 CCATGACGCGCACTGGGCGCAGAGCGCGGCTTCTCATCTCTGCGGTTCTCCAAAGC 300
Db      241 CCATGACGCGCACTGGGCGCAGAGCGCGGCTTCTCATCTCTGCGGTTCTCCAAAGC 300
Qy      301 TTGTAACCTTGGCAGAGGCTTGTCTCCGCTGACCTGAGGTTTGTGGCACCAAGACAG 360
Db      301 TTGTAACCTTGGCAGAGGCTTGTCTCCGCTGACCTGAGGTTTGTGGCACCAAGACAG 360
Qy      361 ACTTCTTAATTTTGCATCCCAAGAGATCAACCTTTGAAGAGAGAGTACTGGCAAT 420
Db      361 ACTTCTTAATTTTGCATCCCAAGAGATCAACCTTTGAAGAGAGAGTACTGGCAAT 420

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QY 421 CTCAGTCACCAGGATATTTGCAAAATATGATCCATCCCTCTGATGTGAGAGAAAGT 480
 DB 421 CTCAGTCACCAGGATATTTGCAAAATATGATCCATCCCTCTGATGTGAGAGAAAGT 480
 QY 481 TAGGGTTGGATATGCGCTTACCAAGACAAATTCCTACCTCCAGAGACAATAACGAAAAAGT 540
 DB 481 TAGGGTTGGATATGCGCTTACCAAGACAAATTCCTACCTCCAGAGACAATAACGAAAAAGT 540
 QY 541 TCAAGAACAGCACTACTCAAGAGCTGTGATGATGTGATATCACTTTGGCAAACTGCT 600
 DB 541 TCAAGAACAGCACTACTCAAGAGCTGTGATGATGTGATATCACTTTGGCAAACTGCT 600
 QY 601 CAGGACTGGACTTGAATCTTTGGCTTAATGCGCTTAATTAAGAACAGCAGATTTGCACTGGA 660
 DB 601 CAGGACTGGACTTGAATCTTTGGCTTAATGCGCTTAATTAAGAACAGCAGATTTGCACTGGA 660
 QY 661 ACAGTTCTAATGCTCAAGTTGCTCTGAGACTAGCTCTTCCAAAGGGATTAACATTTCTT 720
 DB 661 ACAGTTCTAATGCTCAAGTTGCTCTGAGACTAGCTCTTCCAAAGGGATTAACATTTCTT 720
 QY 721 GGGAACTGAGGAAATGAACCTAACATTTCCCTTAAGAGGCTGATATTTTCAATCAATGGGT 780
 DB 721 GGGAACTGAGGAAATGAACCTAACATTTCCCTTAAGAGGCTGATATTTTCAATCAATGGGT 780
 QY 781 CGCAGTTAGAGAAATTAATTAATTCATATGATGATTAACCTTAAAGAAAGTCCACCTTCAAAA 840
 DB 781 CGCAGTTAGAGAAATTAATTAATTCATATGATGATTAACCTTAAAGAAAGTCCACCTTCAAAA 840
 QY 841 ATGCAAACTCTATGCTCTGATGTTGGTCACTCTCGAAGAAAGACGCTAAGATGCTGA 900
 DB 841 ATGCAAACTCTATGCTCTGATGTTGGTCACTCTCGAAGAAAGACGCTAAGATGCTGA 900
 QY 901 AGAGCTTCTGAGGCTGCTGAGGAGATGATGATTAATGATGATCAATGATGATGATGATGAT 960
 DB 901 AGAGCTTCTGAGGCTGCTGAGGAGATGATGATTAATGATGATGATGATGATGATGATGAT 960
 QY 961 TGAATGAGACGAGCTCTACCAAGGAAAGATTTTCTAAACCTGATGATGATGATGATGATGAT 1020
 DB 961 TGAATGAGACGAGCTCTACCAAGGAAAGATTTTCTAAACCTGATGATGATGATGATGATGAT 1020
 QY 1021 TTTCAATCTGTGCAAAAAGTTTTCAGGTGTTGAGAGACAGGCTGAGCAAGAAAGTCT 1080
 DB 1021 TTTCAATCTGTGCAAAAAGTTTTCAGGTGTTGAGAGACAGGCTGAGCAAGAAAGTCT 1080
 QY 1081 GGTAGGAGAAACAGCTCTGATATGAGAGGCGGAGCCCTTCTGATTCGACACCTTTG 1140
 DB 1081 GGTAGGAGAAACAGCTCTGATATGAGAGGCGGAGCCCTTCTGATTCGACACCTTTG 1140
 QY 1141 CAGCTGGCTTTATGTGCTGATTAATTTGGGCTGTCAAGCCGAGTGGGAATGAAAGTGG 1200
 DB 1141 CAGCTGGCTTTATGTGCTGATTAATTTGGGCTGTCAAGCCGAGTGGGAATGAAAGTGG 1200
 QY 1201 TGATGAGGCAAGTATTTCTTTGGAGCAGGAACTACCATTTAGTGAATGAAACCTTCGATC 1260
 DB 1201 TGATGAGGCAAGTATTTCTTTGGAGCAGGAACTACCATTTAGTGAATGAAACCTTCGATC 1260
 QY 1261 CTTTACCTGATTAATTTGGCTATCTCTTCTGTTCAAGAAATTTGGTGGCACCAAGGTGTTAA 1320
 DB 1261 CTTTACCTGATTAATTTGGCTATCTCTTCTGTTCAAGAAATTTGGTGGCACCAAGGTGTTAA 1320
 QY 1321 TGGCAAGGCTGCAAGGTTCAAGAGAGAGAGCTTCGAGTATACCTTCATTTGCACAAA 1380
 DB 1321 TGGCAAGGCTGCAAGGTTCAAGAGAGAGAGCTTCGAGTATACCTTCATTTGCACAAA 1380
 QY 1381 CTGACAAATCCAAAGTATTAAGAGAGATTTAACTCTGTATGCAATTAACCTTCATTAACG 1440
 DB 1381 CTGACAAATCCAAAGTATTAAGAGAGATTTAACTCTGTATGCAATTAACCTTCATTAACG 1440
 QY 1441 TCACCAAGGACTTGGGGTTAACCTTATCCCTTTTCAACAAGAAATGATGATTAATCTTC 1500
 DB 1441 TCACCAAGGACTTGGGGTTAACCTTATCCCTTTTCAACAAGAAATGATGATTAATCTTC 1500
 QY 1501 TAAAGACTTTGGGACCTCATGATTAATTTCAAAATCTGTCCAACTCAATGATGATTAATCT 1560

DB 1501 TAAAGCTTTGGGACCTCATGATTAATCTTCAAAATCTGTCCAACTCAATGATGATTAATCT 1560
 QY 1561 TAAAGTGTGTGATGATTAACCTTTGCCACCTTTTAATGAGAAAACTTCCGGCCAGAGAA 1620
 DB 1561 TAAAGTGTGTGATGATTAACCTTTGCCACCTTTTAATGAGAAAACTTCCGGCCAGAGAA 1620
 QY 1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTATAGAAATGCAAAAGTTG 1680
 DB 1621 GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTATAGAAATGCAAAAGTTG 1680
 QY 1681 CTGCTGCATCTGAATAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1721
 DB 1681 CTGCTGCATCTGAATAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1721
 RESULT 12
 AAX35650
 ID AAX35650 standard; cDNA; 1899 BP.
 AC AAX35650;
 DT 09-JUL-1999 (first entry)
 DE CDNA encoding a human heparanase protein.
 KW Heparanase; hpa; modulator; heparin-binding growth factor;
 KW cellular response; cytokine; cell interaction; plasma lipoprotein;
 KW cellular susceptibility; infection; integration;
 KW neurodegenerative plaque; wound healing; angiogenesis; restenosis;
 KW atherosclerosis; inflammation; neurodegenerative disease; neuritis;
 KW plasma heparin; micrometastasis; autoimmune lesion; renal failure; ss.
 OS Homo sapiens.
 PN MO9911798-A1.
 PD 11-MAR-1999.
 PF 31-AUG-1998; 98WO-US017954.
 PR 02-SEP-1997; 97US-00922170.
 PR 02-JUL-1998; 98US-00109386.
 PA (INSI-) INSIGHT STRATEGY & MARKETING LTD.
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 PA (FRIE-) FRIEDMAN M M.
 PI Pecker I, Vlodevsky I, Feinstein E;
 DR WPI; 1999-302255/25.
 DR P-PSDB; AAY02346.
 PT New human polynucleotide useful for treating angiogenesis, restenosis,
 PT and inflammation.
 PS Claim 4; Page 64-65; 63pp; English.
 CC The specification describes a polypeptide having heparanase (hpa)
 CC activity. The recombinant protein is used as a modulator of heparin-
 CC binding growth factors, cellular responses to heparin-binding growth
 CC factors and cytokines, cell interaction with plasma lipoproteins,
 CC cellular susceptibility to viral, protozoal and bacterial infections or
 CC disintegration of neurodegenerative plaques. Heparanase may be useful for
 CC conditions such as wound healing, angiogenesis, restenosis,
 CC atherosclerosis, inflammation, neurodegenerative diseases, and viral
 CC infections. Mammalian heparanase can be used to neutralize plasma
 CC heparin, and anti-heparanase antibodies may be applied for
 CC immunodetection and diagnosis of micrometastases, autoimmune lesions, and
 CC renal failure in biopsy specimens, plasma samples, and body fluids. The
 CC present sequence encodes human heparanase
 SQ Sequence 1899 BP; 495 A; 433 C; 510 G; 461 T; 0 U; 0 Other;

QY	1	CTAAGACTTTGCACTCTCCGCTGCGCCGCACTGGCGGGGGAGCAAGCAAGTGAAGCCA	60
Db	179	CTAGAGCTTCAACTCTCCGCTGCGCCGCAAGTGGCGGGGGAGCAAGCAAGTGAAGCCA	238
QY	61	AATCTCTGCTGCGCTCGAAGCTGTGCTGCGCGCGCTGATCTGTCTCTGGAGGC	120
Db	239	AATCTCTGCTGCGCTCGAAGCTGTGCTGCGCGCGCTGATCTGTCTCTGGAGGC	289
QY	121	CGCTGGATCCCTCTCCGCCCTGGCCCTGCCCCGACCTGCGCAAGCAGAGAGCTGTG	180
Db	299	CGCTGGATCCCTCTCCGCCCTGGCCGCCCTGCCCCGACCTGCGCAAGCAGAGAGCTGTG	358
QY	181	ACCTGGACTTTTTCACCCAGAGAGCGCTGACCTGATGAGCCCCGTGTTCTCTGTCGTC	240
Db	359	ACCTGGACTTTTTCACCCAGAGAGCGCTGACCTGATGAGCCCCGTGTTCTCTGTCGTC	418
QY	241	CCATTGACGCAACCTGGCCACGGACCCCGGGTTCCTCAATCTCTGAGTTCTCCAAAGC	300
Db	419	CCATTGACGCAACCTGGCCACGGACCCCGGGTTCCTCAATCTCTGAGTTCTCCAAAGC	478
QY	301	TTCTGACCTTGGCCAGAGGCTTGTCTCTCTGTAACCTGAGGTTTGGTGGCACAAGACG	360
Db	479	TTCTGACCTTGGCCAGAGGCTTGTCTCTCTGTAACCTGAGGTTTGGTGGCACAAGACG	538
QY	361	ACTTCCTAATTTTTCGATCCCAAGAGGAATCAACTTTGAAGAGAGATTACTGCAAT	420
Db	539	ACTTCCTAATTTTTCGATCCCAAGAGGAATCAACTTTGAAGAGAGATTACTGCAAT	598
QY	421	CTCAAGTCACCGAGATTTTTCGAAATATGATTCATCCCTCTGATGTGAGAGGAAT	480
Db	599	CTCAAGTCACCGAGATTTTTCGAAATATGATTCATCCCTCTGATGTGAGAGGAAT	658
QY	481	TACGTTGGAAATGGCCCTTACAGAGACCAATTCCTACCGAAGACATCCAGAAAAGT	540
Db	659	TACGTTGGAAATGGCCCTTACAGAGACCAATTCCTACCGAAGACATCCAGAAAAGT	718
QY	541	TCAAGACAGCACCTTCTCAAGAAAGCTGTGATGTGTATACACTTTTGCAAACTGCT	600
Db	719	TCAAGACAGCACCTTCTCAAGAAAGCTGTGATGTGTATACACTTTTGCAAACTGCT	778
QY	601	CAGAGCTGACCTTGAATCTTTGGCCTTAATAGGCTTATTAAGAACAGCAATTTGCAATGCA	660
Db	779	CAGAGCTGACCTTGAATCTTTGGCCTTAATAGGCTTATTAAGAACAGCAATTTGCAATGCA	838
QY	661	AAGATTCAATATCTCAATGTTGCTCTGACATCTGTCTTCCAGGGGATTAACATTTCTT	720
Db	839	AAGATTCAATATCTCAATGTTGCTCTGACATCTGTCTTCCAGGGGATTAACATTTCTT	898
QY	721	GGGAACCTAGCAATGAACTTAACAGTTTCTTAAGAGGGCGATATTTTCACTAATGGT	780
Db	899	GGGAACCTAGCAATGAACTTAACAGTTTCTTAAGAGGGCGATATTTTCACTAATGGT	958
QY	781	CGCAATTGAGGAAGATTATTAATTAATGTCATAAATCTTAAGAAAGTCCACCTTCAAAA	840
Db	959	CGCAATTGAGGAAGATTATTAATTAATGTCATAAATCTTAAGAAAGTCCACCTTCAAAA	1018
QY	841	ATGCAAAACTCTATGTCTGATGTTGGTCAAGCTGCAAGAAAGACGGCTTAAGATCTGA	900
Db	1019	ATGCAAAACTCTATGTCTGATGTTGGTCAAGCTGCAAGAAAGACGGCTTAAGATCTGA	1078
QY	901	AGACCTTCTGAAGAGCGCTGTGAGAAATGATTTGATTCAGTTACATGAGCATCACTATAT	960
Db	1079	AGACCTTCTGAAGAGCGCTGTGAGAAATGATTTGATTCAGTTACATGAGCATCACTATAT	1138
QY	961	TGAATGAGCGGACTCTTACACGAGGAAGATTTTCTAAACCCTGATGTGATTTGCAATTTT	1020
Db	1139	TGAATGAGCGGACTCTTACACGAGGAAGATTTTCTAAACCCTGATGTGATTTGCAATTTT	1198

QY	1021	TTTCATCTTGCAAAAAGTTTTCAGAGGTGTGAGAGCACAGGCGCTGCAAGAAGTCT	1080
Db	1199	TTTCATCTTGCAAAAAGTTTTCAGAGGTGTGAGAGCACAGGCGCTGCAAGAAGTCT	1258
QY	1081	GGTTAGAGAAAACAAGCTCGCACTATGAGAGGGGAGGCCCTTGGTATCCGACACTTTG	1140
Db	1259	GGTTAGAGAAAACAAGCTCGCACTATGAGAGGGGAGGCCCTTGGTATCCGACACTTTG	1318
QY	1141	CAGCTGGCTTATGTGGCTGATAAATTGGGCTGTCAGCCGGAATGGAAATAGAAGTGG	1200
Db	1319	CAGCTGGCTTATGTGGCTGATAAATTGGGCTGTCAGCCGGAATGGAAATAGAATGG	1378
QY	1201	TGATGAGCAAGATATCTTTGGAGAGAGAACTACATTTTGTGTAGTAAACTTGCATC	1260
Db	1379	TGATGAGCAAGATATCTTTGGAGAGAGAACTACATTTTGTGTAGTAAACTTGCATC	1438
QY	1261	CTTTACCTGATATTATGGCTATCTCTTCTGTTCAAGAAATTGGTGGGCAACGAGTGTAA	1320
Db	1439	CTTTACCTGATATTATGGCTATCTCTTCTGTTCAAGAAATTGGTGGGCAACGAGTGTAA	1498
QY	1321	TGGCAAGCGTGGCAAGGTTCAAGAGAGAGAACTTCAGATATACCTTCATTGCAAAACA	1380
Db	1499	TGGCAAGCGTGGCAAGGTTCAAGAGAGAGAACTTCAGATATACCTTCATTGCAAAACA	1558
QY	1381	CTGACATTCCAAGGTATAAAGAGAGATTTAACTCTGATGCGCATTAACCTGCATPAG	1440
Db	1559	CTGACATTCCAAGGTATAAAGAGAGATTTAACTCTGATGCGCATTAACCTGCATPAG	1618
QY	1441	TCACCAAGTATCTGGGGTTACCCATACCTTTCTTAACAAGCAAGTGATTAATACCTTC	1500
Db	1619	TCACCAAGTATCTGGGGTTACCCATACCTTTCTTAACAAGCAAGTGATTAATACCTTC	1678
QY	1501	TAAAGCTTTGGGAGCTCATGATTACTTTCCAAATCTGTCCAACCTCAATGGTCAACTC	1560
Db	1679	TAAAGCTTTGGGAGCTCATGATTACTTTCCAAATCTGTCCAACCTCAATGGTCAACTC	1738
QY	1561	TAAAGATGGAGATGATCAACAACCTTGGCACCTTTAATGGAAAAACCTTCGCGCAGGAA	1620
Db	1739	TAAAGATGGAGATGATCAACAACCTTGGCACCTTTAATGGAAAAACCTTCGCGCAGGAA	1798
QY	1621	GTTCACTGGGCTTGCACAGCTTTCATATAGTATTTTGTGATAGAAATGCAAAAGTTG	1680
Db	1799	GTTCACTGGGCTTGCACAGCTTTCATATAGTATTTTGTGATAGAAATGCAAAAGTTG	1858
QY	1681	CTGCTTGCATCTGAAAAATAAATATATCTATGTCCTGACACTG 1721	
Db	1859	CTGCTTGCATCTGAAAAATAAATATATCTATGTCCTGACACTG 1899	

	RESULT	13
AAAT75053	ID	AAAT75053 standard; cDNA, 1899 BP.
XX	AC	AAA75053;
XX	DT	15-JAN-2001 (first entry)
XX	DE	cDNA encoding a human heparanase polypeptide.
XX	KW	Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
KW	KM	heparin-binding growth factor; cytokine; neurodegenerative plaque;
KW	KW	wound healing; infection; burn; angiogenesis; restenosis;
KX	KW	atherosclerosis; inflammation; neurodegenerative disease;
XX	KW	Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; ds.
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
FH	CDS	94..1872
FT		/*tag= a
FT	/product=	"heparanase"
XX		
XX		

XX 08-SEP-2000.
PD
XX 14-FEB-2000; 2000MO-US003542.
PF
XX 01-MAR-1999; 99US-00258892.
PR
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.
XX
PI Pecker I, Vlodavsky I, Feinstein E;
XX
DR WPI: 2000-579289/54.
DR P-PSDB; AAB08850.
XX
PT New polynucleotides encoding a polypeptide having heparanase activity,
PT useful in wound healing and in gene therapy, particularly in treating
PT tumor, inflammation, autoimmunity, neurodegenerative diseases.
XX
PS Claim 9; Page 121-122; 152pp; English.
XX
XX The present sequence encodes a human protein with heparanase catalytic
CC activity. The heparanase (hpa) polynucleotide is useful in gene therapy,
CC particularly in treating tumour, inflammation or autoimmunity.
CC Particularly, the polynucleotide is useful in modulating the
CC bioavailability of heparin-binding growth factors, cellular responses to
CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
CC Interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular
CC susceptibility to certain viral and some bacterial and protozoa
CC infections, or disintegration of neurodegenerative plaques. The
CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
CC radiation burns), and in the treatment of angiogenesis, restenosis,
CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
CC Strausler Syndrome or Creutzfeldt-Jakob disease), and some viral,
CC bacterial or protozoa infections
CC
SQ Sequence 1899 BP; 495 A; 433 C; 510 G; 461 T; 0 U; 0 Other;
Query Match 99.9%; Score 1719.4; DB 3; Length 1899;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTAGAGCTTTGACCTCCGCTGCGCGGAGCTGGCGGGGAGAGCAGGTGAGCCCA 60
DB 179 CTAGAGCTCTGACCTCTCCGCTGCGCGGAGCTGGCGGGGAGAGCAGGTGAGCCCA 238
QY 61 AGATGCTGCTGCGCTCGAAGCTTGCGCTGCGCGCGCTGATGCTGCTGCTGAGGC 120
DB 239 AGATGCTGCTGCGCTCGAAGCTTGCGCTGCGCGCGCTGATGCTGCTGCTGAGGC 298
QY 121 CGCTGGGTCCTCTCTCCCTGCGCGCTGCGCGCGAGCTTGCGGACACAGAGCTGCG 180
DB 299 CGCTGGGTCCTCTCTCCCTGCGCGCTGCGCGCGAGCTTGCGGACACAGAGCTGCG 358
QY 181 ACCTGAGCTTTCTTCAACCGAGGACCGCTGCACTGTGAGCCCCCTCTCTCTCTCTCA 240
DB 359 ACCTGAGCTTTCTTCAACCGAGGACCGCTGCACTGTGAGCCCCCTCTCTCTCTCTCA 418
QY 241 CCATTGAGCGCAACCTGCGCAGGACCGCGGTTCTCTCATCTCTGAGGTTTCCAAAGC 300
DB 419 CCATTGAGCGCAACCTGCGCAGGACCGCGGTTCTCTCATCTCTGAGGTTTCCAAAGC 478
QY 301 TTGCTGACCTTGGCGCAGAGGCTTGTCTCTGCTGACCTGAGGTTGTGTGCGCACCAAGC 360
DB 479 TTGCTGACCTTGGCGCAGAGGCTTGTCTCTGCTGACCTGAGGTTGTGTGCGCACCAAGC 538
QY 361 ACTTGCTAATTTTGCATCCCAAGAGAAATCACTTTGAGAGAGAGATTATCGGCAT 420
DB 539 ACTTGCTAATTTTGCATCCCAAGAGAAATCACTTTGAGAGAGAGATTATCGGCAT 598
QY 421 CTCAGTCAACCAAGATATTTGCAATATGATTCATCCCTCTGATGTGAGAGAAAGT 480

DB 599 CTCAGTCAACCAAGATATTTGCAATATGATTCATCCCTCTGATGTGAGAGAAAGT 658
QY 481 TACGTTGGAATTTGACCCCTACACAGAGCAATTTGCTCCGAGACATCAACAGAAAAGT 540
DB 659 TACGTTGGAATTTGACCCCTACACAGAGCAATTTGCTCCGAGACATCAACAGAAAAGT 718
QY 541 TCAAGAACAGCACTTACAGAGAGCTCTGAGATGTCATACATCTTTTCCAACTGCT 600
DB 719 TCAAGAACAGCACTTACAGAGAGCTCTGAGATGTCATACATCTTTTCCAACTGCT 778
QY 601 CAGGACTGGAATTTGAGCTTAAAGGCTTAAATGAGAACAGCAGATTTGCAAGTGA 660
DB 779 CAGGACTGGAATTTGAGCTTAAAGGCTTAAATGAGAACAGCAGATTTGCAAGTGA 838
QY 661 ACAGTTCTAATGCTCAGTTGCTCTGAGCTATCTGCTCTTCCAAAGGGAATTAATTTCTT 720
DB 839 ACAGTTCTAATGCTCAGTTGCTCTGAGCTATCTGCTCTTCCAAAGGGAATTAATTTCTT 898
QY 721 GGGAACTGAGCAATGAACCTTACAGTTTCTTAAAGAGGCTGATATTTTCATCATGGGT 780
DB 899 GGGAACTGAGCAATGAACCTTACAGTTTCTTAAAGAGGCTGATATTTTCATCATGGGT 958
QY 781 CGCAGTTAGAGAAAGATTATATTCATATTCATTAACCTTAAAGAGTCCACTTCAAA 840
DB 959 CGCAGTTAGAGAAAGATTATATTCATATTCATTAACCTTAAAGAGTCCACTTCAAA 1018
QY 841 ATGCAAACTTATGCTCTGATGTTGTGCTGAGCTTCCAGAGAAAGCGCTTAAGTGTGA 900
DB 1019 ATGCAAACTTATGCTCTGATGTTGTGCTGAGCTTCCAGAGAAAGCGCTTAAGTGTGA 1078
QY 901 AGAGCTTCTGAAGGCTGAGAGAGATTTGAATTCAGTTACATGAGCACTACTATTT 960
DB 1079 AGAGCTTCTGAAGGCTGAGAGAGATTTGAATTCAGTTACATGAGCACTACTATTT 1138
QY 961 TGAATGAGCGGACTCTACACAGGAGATTTTCTAAACCTGATGATTTGACATTTTAA 1020
DB 1139 TGAATGAGCGGACTCTACACAGGAGATTTTCTAAACCTGATGATTTGACATTTTAA 1198
QY 1021 TTTTCACTGTGCAAAAAGTTTTCAGAGTGTGAGAGACACAGGCTTGGCAAGAGTCT 1080
DB 1199 TTTTCACTGTGCAAAAAGTTTTCAGAGTGTGAGAGACACAGGCTTGGCAAGAGTCT 1258
QY 1081 GGTTAGAGAAACAAGCTCTGCATATGAGAGCGAGCGCTTGTCTATCCGACACTTTG 1140
DB 1259 GGTTAGAGAAACAAGCTCTGCATATGAGAGCGAGCGCTTGTCTATCCGACACTTTG 1318
QY 1141 CAGCTGCTTTATGTGCTGATTAATTTGGCTGTCAAGCCGATGAGAAATGAAAGTGG 1200
DB 1319 CAGCTGCTTTATGTGCTGATTAATTTGGCTGTCAAGCCGATGAGAAATGAAAGTGG 1378
QY 1201 TGATGAGCAAGTATTTCTTGGAGCAGAAATCACTATTTAGTGAATGAAATTTCCATC 1260
DB 1379 TGATGAGCAAGTATTTCTTGGAGCAGAAATCACTATTTAGTGAATGAAATTTCCATC 1438
QY 1261 CTTTACCGATTATTTGGCTATCTCTCTGTCAAGAAATGAGTGGGACCAAGGTTTAA 1320
DB 1439 CTTTACCGATTATTTGGCTATCTCTCTGTCAAGAAATGAGTGGGACCAAGGTTTAA 1498
QY 1321 TGGCAAGGCTCAAGGTTCAAGAGAAAGAGCTTCAAGTATACCTTATTTGCACAAA 1380
DB 1499 TGGCAAGGCTCAAGGTTCAAGAGAAAGAGCTTCAAGTATACCTTATTTGCACAAA 1558
QY 1381 CTGACATCCAAAGTATTAAGAAAGATTTAATCTGTATAGCCATTAACCTTCCATACG 1440
DB 1559 CTGACATCCAAAGTATTAAGAAAGATTTAATCTGTATAGCCATTAACCTTCCATACG 1618
QY 1441 TCACCAAGTACTTGGGTTACCTATCTTTTCTTAAACAAGTGAATTAATCTTTC 1500
DB 1619 TCACCAAGTACTTGGGTTACCTATCTTTTCTTAAACAAGTGAATTAATCTTTC 1678
QY 1501 TAAAGCTTTGGGACCTCATGAGATTAATTTCCAAATCTGTCCAACTCAATGCTTAACTC 1560
DB 1679 TAAAGCTTTGGGACCTCATGAGATTAATTTCCAAATCTGTCCAACTCAATGCTTAACTC 1738

RESULTS	14
ADG88803	
ID	ADG88803 standard; cDNA; 1899 BP.
XX	
XX	ADG88803;
AC	
XX	
XX	
DT	11-MAR-2004 (first entry)
XX	
DE	Human SK-hep1 cDNA.
XX	
XX	
KW	Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
KW	necrosis; pressure wound; diabetic ulcer; angiogenesis; human; therapy
KW	Gene; ss.
XX	
XX	
XX	Homo sapiens.

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Location/Qualifiers
94. .1872
/*tag= a
/product= "Human SK-hep1 protein"
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US2003161823-A1.

28-AUG-2003

14-JAN-2003; 2003US-00341582.

31-AUG-1998; 98WO-US017954.

06-FEB-2001; 2001US-00776874.

19-NOV-2001; 2001US-00988113.

(ILAN/) ILAN N.
(VIAD/) VIADAVICIA -

(YACO/) YACOBY-ZEEVI O.
(DECK /) DECKED T

(FEIN/) FEINSTEIN E.

Ilan N, Vlodavsky I, Yacoby

WPI; 2003-897910/82.
P-PSDB: ADG88804

Composition for treating a no

useful to induce or accelerate angiogenesis.

Claim 4; SEO ID NO 13: 143pp.

The present invention relates

and/or accelerating wound healing/heparanase. The invention is a

necrosis, pressure wound, dial

ing-voicings: the present beq

Sequence 1899 BP; 495 A; 433 C

100

Query Match	99.9%	Score 1719.4;	DB 10;	Length 1899;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1720; Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;

QY	1	CTAAGGCTTTCGACTCTCCGCTGCGGCACTGCGCGGGGAGCAGCCAGGTGAACCCA	60
Db	179	CTAAGGCTCTGACTCTCCGCTGCGGGAAGCTGGGGGGGAGAGCAGGTGAGGCCA	238
QY	61	AGATGCTGCTGCGCTCGAAGCTGCGCTCGCGCGCGCTGAATGCTGCGCTCGGGGGC	120
Db	239	AGATGCTGCTGCGCTCGAAGCTGCGGCTGCGCGCGCGCTGATGCTGCTCTGGGGGC	298
QY	121	CGCGGGGTCCCTCTCCCTCGGCGCCTTGCCCCGACCTGCGCAGACAGGAGCTGCG	180
Db	299	CGCTGGGTCCCTCTCTCCCTGCGCGCTGCGCCGACCTGCGCAGACAGGAGCTGCGG	358
QY	181	ACCTGACCTTCTTCAACCCAGAGCGGCTGACCTGGTAGGCGCCCTCGTCTGTGCGGCA	240
Db	359	ACCTGGACTTCTTCAACCCAGAGCGGCTGACCTGGTAGGCGCCCTCGTCTGTGCGGCA	418
QY	241	CCATTGACCGCAACCTGGGCGACAGGACCCGCGGTTCTTCACTCTCTGAGTTCTCAAGC	300
Db	419	CCATTGACCGCAACCTGGGCGACAGGACCCGCGGTTCTTCACTCTCTGAGTTCTCAAGC	478
QY	301	TTTGTAACCTTGGCCAGAGGCTTGCTCCGCGTACTGAGGTTTGATGGGACCAAGCAG	360
Db	479	TTTGTAACCTTGGCCAGAGGCTTGCTCCGCGTACTGAGGTTTGATGGGACCAAGCAG	538
QY	361	ACTTCCCTAATTTTGAATCCCAAGAAAGAAATCACTTTGAAGAGAGATTTACTGGCAAT	420
Db	539	ACTTCCCTAATTTTGAATCCCAAGAAAGAAATCACTTTGAAGAGAGATTTACTGGCAAT	598
QY	421	CTCAAGTCACACGAGATATTTGCAATATAGATTCATCCCTCGATGTGAGAGAGAACT	480
Db	599	CTCAAGTCACACGAGATATTTGCAATATAGATTCATCCCTCGATGTGAGAGAGAACT	658
QY	481	TACGGTTGGAATGGGCCCTACACGAGAGAAATGCTACTCCGAGAAACACTACAGAAAAAGT	540
Db	659	TACGGTTGGAATGGGCCCTACACGAGAGAAATGCTACTCCGAGAAACACTACAGAAAAAGT	718
QY	541	TCGAAGACAGCACTTACTCAAGAAAGCTCTGTAGATGTCTATACATTTTGGCAACTGCT	600
Db	719	TCGAAGACAGCACTTACTCAAGAAAGCTCTGTAGATGTCTATACATTTTGGCAACTGCT	778
QY	601	CAGGACTGGACTTGATCTTTGGCCCTAAATGCGTTATTAAGAACAGCAATTTGCACTGGA	660
Db	779	CAGGACTGGACTTGATCTTTGGCCCTAAATGCGTTATTAAGAACAGCAATTTGCACTGGA	838
QY	661	ACAATTCTAATGCTCAGTTGCTCTGAGACTATCTTTCAAGGGGTTATACATTTCTT	720
Db	839	ACAATTCTAATGCTCAGTTGCTCTGAGACTATCTTTCAAGGGGTTATACATTTCTT	898
QY	721	GGGAACTAGGCAATGAACCTTAACAGTTTCTTAAGAAAGGCTGATTTTTCATCAATGGGT	780
Db	899	GGGAACTAGGCAATGAACCTTAACAGTTTCTTAAGAAAGGCTGATTTTTCATCAATGGGT	958
QY	781	CGCAGTTAGAGAAAGATATATTCATTAATTCATTAACCTTCTAAGAAAGTCAACTTCAAAA	840
Db	959	CGCAGTTAGAGAAAGATATATTCATTAATTCATTAACCTTCTAAGAAAGTCAACTTCAAAA	1018
QY	841	ATGCAAAAACCTATGATCCCTGATGTTGGTCAACCTCGAAGAAAGCGGCTTAAGTGTCTGA	900
Db	1019	ATGCAAAAACCTATGATCCCTGATGTTGGTCAACCTCGAAGAAAGCGGCTTAAGTGTCTGA	1078
QY	901	AGAGCTTTCCTGAAGGCTGGTGGAGAAAGTATTCAGTTACATGCGATCACTACTATT	960
Db	1079	AGAGCTTTCCTGAAGGCTGGTGGAGAAAGTATTCAGTTACATGCGATCACTACTATT	1138
QY	961	TGAATGAGACGACTGCTACAGGAGAAAGTTTCTAAACCCGATGATTTGAGACATTTTGA	1020
Db	1139	TGAATGAGACGACTGCTACAGGAGAAAGTTTCTAAACCCGATGATTTGAGACATTTTGA	1198
QY	1021	TTTCAATCTGTGCAAAAAGTTTTTCCAGGTGTTGAGAGCACCGAGCTGCGCAAGAGGTCCT	1080

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Db      1199  TTTTCATCTGTGCAAAAAGTTTCCAGGTGCTGAGAGCACCAGGCTGGCAAGAGTCT 1258
Qy      1081  GGTGAGGAAACAAGCTCTGTGATATGAGGGGGAGCCGCTTGTATCCGACACTTGG 1140
Db      1259  GGTGAGGAAACAAGCTCTGTGATATGAGGGGGAGCCGCTTGTATCCGACACTTGG 1318
Qy      1141  CAGTGGCTTATATGTGCTGATATTAATTGGGCTCTCAGCCGGAATGGGAATAGAATGG 1200
Db      1319  CAGTGGCTTATATGTGCTGATATTAATTGGGCTCTCAGCCGGAATGGGAATAGAATGG 1378
Qy      1201  TGATGAGCAAGATATTTCTTGGAGAGAACTACCATTTAGTGTATGAAAATTGATC 1260
Db      1379  TGATGAGCAAGATATTTCTTGGAGAGAACTACCATTTAGTGTATGAAAATTGATC 1438
Qy      1281  CTTTACCTGATATTTGGCTATCTCTTCTGTCAAGAAATGGTGGGACCAAGGTGTTA 1320
Db      1439  CTTTACCTGATATTTGGCTATCTCTTCTGTCAAGAAATGGTGGGACCAAGGTGTTA 1498
Qy      1321  TGGCAAGGCTGCAAGGTTCAAGAGAGAGAGCTTCAGATATACCTTCATTTGCAAAACA 1380
Db      1439  TGGCAAGGCTGCAAGGTTCAAGAGAGAGAGCTTCAGATATACCTTCATTTGCAAAACA 1558
Qy      1391  CTGACAATCCAAAGGTATATAAGAGAGATTTAATCTGTATGCAATAAACCCTCCATAACG 1440
Db      1559  CTGACAATCCAAAGGTATATAAGAGAGATTTAATCTGTATGCAATAAACCCTCCATAACG 1618
Qy      1441  TCACCAAGTACTTGGGGTTACCTTATCCTTTTTCACCAAGAGAGATGATTAATACCTTC 1500
Db      1619  TCACCAAGTACTTGGGGTTACCTTATCCTTTTTCACCAAGAGAGATGATTAATACCTTC 1678
Qy      1501  TAAAGACTTTGGGAGCTCATGATGATTACTTCCAAATCTGCCAATCAATGCTCAATC 1560
Db      1679  TAAAGACTTTGGGAGCTCATGATGATTACTTCCAAATCTGCCAATCAATGCTCAATC 1738
Qy      1561  TAAAGATGATGATGATCAAAACCTTGCCACCTTTATGGAAGAAACCTTCGCGCCAGAGAA 1620
Db      1739  TAAAGATGATGATGATCAAAACCTTGCCACCTTTATGGAAGAAACCTTCGCGCCAGAGAA 1798
Qy      1621  GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAGAAATGCGAAAGTTG 1680
Db      1799  GTTCACTGGGCTTGGCAGCTTCTCATATAGTTTTTTTGTGATAGAAATGCGAAAGTTG 1858
Qy      1681  CTGCTTGATCTGAATAATAATATATAGTCTGACACTG 1721
Db      1859  CTGCTTGATCTGAATAATAATATATAGTCTGACACTG 1899

RESULT 15
ADG88805
ID      ADG88805 standard; cDNA; 1899 BP.
AC      ADG88805;
XX      11-MAR-2004 (first entry)
XX      Human SK-hep1 cDNA.
XX      Wound healing; heparanase; ulcer; burn; laceration; surgical incision;
XX      neovasis; pressure wound; diabetic ulcer; angiogenesis; human; therapy;
XX      gene; ss.
XX      Homo sapiens.
XX      OS
XX      Key      Location/Qualifiers
XX      CDS      94..1872
XX      FT      /*tag= a
XX      FT      /product= "Human SK-hep1 protein"
XX      PN      US2003161823-A1.
XX      PD      28-AUG-2003.

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PF      14-JAN-2003; 2003US-00341582.
XX      31-AUG-1998; 98WO-US017954.
PR      01-MAR-1999; 99US-00258892.
PR      06-FEB-2001; 2001US-00776874.
PR      05-SEP-2001; 2001WO-1L000830.
PR      19-NOV-2001; 2001US-00988113.
XX      (ILAN/) ILAN N.
XX      (VLAD/) VLADAVSKY I.
XX      (YACO/) YACOBY-ZEEVI O.
XX      (PECK/) PECKER I.
XX      (FEIN/) FEINSTEIN E.
PI      Ilan N, Vladavsky I, Yacoby-Zeevi O, Pecker I, Feinstein E;
DR      WPI: 2003-897910/82.
DB      P-PSDB; ADG88804.
XX      Composition for treating a wound comprising recombinant heparanase is
XX      useful to induce or accelerate wound healing and induce or accelerate
XX      angiogenesis.
XX      Example 6; SEQ ID NO 15; 143bp; English.
XX      The present invention relates to methods and compositions for inducing
XX      and/or accelerating wound healing via the catalytic activity of
XX      heparanase. The invention is used to induce or accelerate a healing
XX      process, particularly of an ulcer, burn, laceration, surgical incision,
XX      necrosis, pressure wound, diabetic ulcer and to induce or accelerate
XX      angiogenesis. The present sequence is human SK-hep1 cDNA.
SQ      Sequence 1899 BP; 495 A; 433 C; 510 G; 461 T; 0 U; 0 Other;
Query Match      99.9%; Score 1719.4; DB 10; Length 1899;
Beet local similarity 99.9%; Pred. No. 0;
Matches 1720; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      1      CTAGAGCTTTCGACTTCCTCCGCTGGCGGCACTGCGGGGGAGACAGCAGTAGAGCCA 60
Db      179      CTAGAGCTTTCGACTTCCTCCGCTGGCGGCACTGCGGGGGAGACAGCAGTAGAGCCA 238
Qy      61      AGATGCTGCTCGCTCGAGCCTGCGTGCAGCCGCGCTGATGCTGCTCTCGGGGC 120
Db      239      AGATGCTGCTCGCTCGAGCCTGCGTGCAGCCGCGCTGATGCTGCTCTCGGGGC 298
Qy      121      CGTGGGTCCTCTCTCCCTGGGCGCTGCGCCGACCTGCGCAAGACAGAGCTGTGG 180
Db      299      CGTGGGTCCTCTCTCCCTGGGCGCTGCGCCGACCTGCGCAAGACAGAGCTGTGG 358
Qy      181      ACTTGAATCTTTTCAACCAAGAGCCGCTGCACTGTGTAGAGCCCTCTGTTCCCTCA 240
Db      359      ACTTGAATCTTTTCAACCAAGAGCCGCTGCACTGTGTAGAGCCCTCTGTTCCCTCA 418
Qy      241      CCATTGACGCAACTGTGGCCACGAGACCGGCTTCTCATCTCTGAGTTCTCAAAAGC 300
Db      419      CCATTGACGCAACTGTGGCCACGAGACCGGCTTCTCATCTCTGAGTTCTCAAAAGC 478
Qy      301      TTGCTACCTTGGCCAGAGGCTTGTCTCTGTGTAATGAGGTTTGTGGACCAAGACAG 360
Db      479      TTGCTACCTTGGCCAGAGGCTTGTCTCTGTGTAATGAGGTTTGTGGACCAAGACAG 538
Qy      361      ACTTCTTAATTTTGTGATCCCAAGAGAAATCAACTTTTGAAGAGAAATTAATGGCAAT 420
Db      539      ACTTCTTAATTTTGTGATCCCAAGAGAAATCAACTTTTGAAGAGAAATTAATGGCAAT 598
Qy      421      CTCAAGTCAACCAAGATATTTGCAAAATATGATCCATCCCTGATGTGGAGAGAAAGT 480
Db      599      CTCAAGTCAACCAAGATATTTGCAAAATATGATCCATCCCTGATGTGGAGAGAAAGT 658
Qy      481      TACGGTTGGAATGGCCCTTACCAAGAGCAATTTGTAATCTCCAGAAACCTACCAAGAAAGT 540
Db      659      TACGGTTGGAATGGCCCTTACCAAGAGCAATTTGTAATCTCCAGAAACCTACCAAGAAAGT 718

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